

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: February 27, 2003, 05:13:08 : Search time 56 Seconds
(without alignments)
3543.212 Million cell updates/sec

Title: US-09-677-653A-50

Perfect score: 3374
Sequence: 1 MGDAQVASQRPNNRGRTRNV.....GKIAKRVARRARRARRAAN 647

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 segs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+gpn.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09677653/rnucat_20022003_164315_1277/app-query.fasta_1.839
-DB=Issued Patents_NA -QFMT=fastp -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=humad40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORMTEXT -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09677653 -ECGN_1_1_21_@rnucat_20022003_164315_1277 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMECUT=120
-WARN_TIMECUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents_NA: *
1: /cgn2_6/p2nata/1/lna/5A.COMB.seq: *
2: /cgn2_6/p2nata/1/lna/5B.COMB.seq: *
3: /cgn2_6/p2nata/1/lna/6A.COMB.seq: *
4: /cgn2_6/p2nata/1/lna/6B.COMB.seq: *
5: /cgn2_6/p2nata/1/lna/6C.COMB.seq: *
6: /cgn2_6/p2nata/1/lna/6D.COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3374	100.0	2478	4	US-08-485-355B-47	Sequence 47, Appl
2	3374	100.0	2478	4	US-08-485-355B-49	Sequence 49, Appl
3	3374	100.0	2478	4	US-09-194-613-1	Sequence 1, Appl
4	3361	99.6	2479	4	US-08-485-355B-51	Sequence 51, Appl
5	294	8.7	6534	4	US-09-194-613-4	Sequence 4, Appl
6	139.5	4.1	3695	4	US-09-071-035-419	Sequence 419, App
7	139.5	4.1	3840	4	US-09-071-035-417	Sequence 417, App
8	125.5	3.7	2748	4	US-09-199-290-33	Sequence 33, Appl
9	124	3.7	4403765	4	US-09-103-840A-2	Sequence 2, Appl
10	121	3.6	3833	1	US-08-917-320-18	Sequence 18, Appl
11	121	3.6	3833	5	PCT-US95-04611A-18	Sequence 18, Appl
12	121	3.6	5931	3	US-08-783-774-1	Sequence 1, Appl

C	13	121	3.6	5931	4	US-09-556-706B-1	Sequence 1, Appl
C	14	121	3.6	4403765	4	US-09-103-840A-2	Sequence 2, Appl
C	15	121	3.6	4411529	4	US-09-103-840A-1	Sequence 1, Appl
	16	120	3.6	2798	4	US-09-071-035-415	Sequence 415, App
	17	120	3.6	3078	4	US-09-071-035-413	Sequence 413, App
	18	117.5	3.5	4776	2	US-08-852-401-1	Sequence 1, Appl
	19	117.5	3.5	1803	1	US-08-821-119-18	Sequence 18, Appl
	20	117	3.5	1803	2	US-08-821-118-1	Sequence 1, Appl
	21	117	3.5	3030	4	US-09-268-347-29	Sequence 29, Appl
C	22	117	3.5	30001	1	US-08-125-466-1	Sequence 1, Appl
C	23	117	3.5	30001	2	US-08-474-933-1	Sequence 1, Appl
C	24	116.5	3.5	1929	2	US-08-818-253-1	Sequence 1, Appl
	25	116.5	3.5	1929	2	US-08-818-253-5	Sequence 5, Appl
	26	116.5	3.5	1929	4	US-08-818-252-1	Sequence 1, Appl
	27	116.5	3.5	1929	4	US-08-818-252-5	Sequence 5, Appl
	28	116.5	3.5	1959	2	US-08-818-253-3	Sequence 3, Appl
	29	116.5	3.5	1959	4	US-08-818-252-3	Sequence 3, Appl
	30	116.5	3.5	1971	2	US-08-818-252-7	Sequence 7, Appl
	31	116.5	3.5	1971	4	US-08-818-252-7	Sequence 7, Appl
	32	116	3.4	2451	1	US-07-731-157A-3	Sequence 3, Appl
	33	116	3.4	2451	1	US-08-229-444B-1	Sequence 1, Appl
	34	116	3.4	2451	2	US-08-541-780-3	Sequence 3, Appl
	35	115.5	3.4	3068	2	US-08-224-482-1	Sequence 1, Appl
	36	115.5	3.4	3086	1	US-08-040-548-15	Sequence 15, Appl
	37	115.5	3.4	3086	1	US-08-466-344-15	Sequence 15, Appl
	38	115.5	3.4	3086	6	5206152-1	Sequence 15, Appl
	39	113.5	3.4	25165	4	US-09-453-702B-39	Sequence 39, Appl
C	40	113	3.3	2460	4	US-09-305-681-3	Sequence 3, Appl
C	41	113	3.3	2906	4	US-09-453-702B-186	Sequence 186, App
C	42	112.5	3.3	2923	1	US-08-243-542-6	Sequence 6, Appl
C	43	112.5	3.3	2923	1	US-08-477-407-6	Sequence 6, Appl
C	44	112.5	3.3	2923	1	US-08-484-355-6	Sequence 6, Appl
C	45	112	3.3	4411529	4	US-09-103-840A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-485-355B-47
Sequence 47, Application US/08485355B
Patent No. 6177075
GENERAL INFORMATION:
APPLICANT: Christian, P. D., Gordon, K. H.J., Hanzlik, T. N.
TITLE OF INVENTION: Insect Viruses and Their Uses in
Protecting Plants
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr Hobach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,355B
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,522
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/089,372
FILING DATE: 08-JUL-1993
APPLICATION NUMBER: AU PL4081/92
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Treacartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58631-2/RFT/DSS

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 2478 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

CULE TYPE: DNA

FEATURE:

NAME/KEY: CDS

LOCATION: 283..753

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-08-485-355B-47

Alignment Scores:

```

      0
Length: 2478

```

3374.00	Matches:	647
---------	----------	-----

Similarity: 100.008 Conservative: 0

al Similarity: 100.008 Mismatches: 0

Indels:	0
100.00%	
atch:	

4 Gaps: 0

US-09-677-653A-50 (1-647) x US-08-485-355B-47 (1-2478)

QY	1	MelValAspIaIaGlyValAlaIaSerGlnIaArgProIaIaAsnArgArgIlyThrArgAsnVal	20
Db	366	ATGGAGATCTCTGGAGGGCTGACAGCGACCTCACAAACCGTGGCGAAACCCGTAAAGCTT	425
QY	21	ArgValSerAlaAsnThrValThrValaAngIyArgArgAsnGlnIaArgArgIlyThrGly	40
Db	426	CGGGTCAGCGCCAAACACCGTCACCGTCATGTGGAGAAACCAACGAGGCTGGACCGGA	485
QY	41	ArgGlnValSerProProAspAsnPhetThrAlaAlaIaGlnAspLeuAlaGlnSerLeu	60
Db	486	AGGCAATTTCTCCCTCGCAATTTCCACCGCTGCGCAAGACCTCCGCCAAAGCCCTT	545
QY	61	AspAlaAsnThrValThrPheProAlaAsnIleSerSerMetProGlnPheArgAsnTrp	80
Db	546	GAGCGCCACACCGTCACCTTTCCCGCTAACATCTTCAGCATGCCGAATTCGGGAATTGG	605
QY	81	AlaIaGlyIlyLysIleAspLeuAspSerAspSerIleGlyTrpTrpPheLysTyrLeuAsp	100
Db	606	GCCCAAGGGAAGATTCAGACCTCGACTCCGATTCATCGCTGGTACTTCAAAGTAACTTGAC	665
QY	101	ProAlaGlyValaThrGlnSerAlaArgAlaValaGlyGlyTyrSerLysIleProAspGly	120
Db	666	CCAGCGGGGTCTACAAGTCTGGCGCGCGCGTGGGGAATCTCGAAGTCCCTACAGGC	725
QY	121	LeuValIlyPheSerValAspAlaGlnIleArgGlnIleTyrAsnGlnGluAspProVal	140
Db	726	CTCGTCAAGTTCCTCGTCGACGAGAGATTAAGAGATCTATAAGAGAGATGCCCGCTC	785
QY	141	ValThrAspValSerValProLeuAspGlyArgGlnTrpPheSerLeuSerIlePheSerPhe	160
Db	786	GTCACGTACGACTGTCCCTCCCTCGACGGCGCCGATGGAGGCTCTCGATTTTCTCTTTT	845
QY	161	ProMetPheArgThrAlaTyrValAlaValaIaAsnValaGlnAsnLysGlnMetSerLeu	180
Db	846	CCCATGTTCCGAACCCCTTACGTCGCCCGTAAGGAACGTGGAAGAAAGAGATGTGCGCTC	905
QY	181	AspValValaAsnAspLeuIleGlnTrpLeuAsnAsnLeuAlaAspTrpArgTyrValVal	200
Db	906	GACGTTGTCAAGACCTCATCGATGGGTGCCTCAACAAATCTGCCGACGTGCGATTATCGCTT	965
QY	201	AspSerGlnGlnTrpIleAsnPheThrAsnAspThrThrTyrTyrValArgIleArgVal	220
Db	966	GACTCTGAACAGTGGATTAACTTCAACCATGTACACACAGCTACTACGTCCGATCCGCGCTT	1025
QY	221	LeuArgProThrTyrAspValProAspProThrGlnGlyLeuValArgThrValSerAsp	240

Db	1026	CTACGTCACACTACGACGCTTCCAGACCCCAAGAGAGGCGCTTGTCCGCAACTCTCAGAC	1083
Qy	241	TYrArGLeuThrTYrLYsAlAlLeThrCYsGluAlAsnMeLProThrLeuValAspGln	260
Db	1086	TACCGCGCTCACTATTAAAGCGCATTAACATGTGAAGCCAAACATGCTCGACCA	1145
Qy	261	GLYpHeTrpLlLeGlyGlyGlnTYrAlAlaLeuThrProThrSerLeuProGlnTYrAspAl	280
Db	1146	GGCTTTGGATCGGGGCGCAGTACGCTCCACCCGCACTAGCTCAACCGAGTACAGCGTC	1205
Qy	281	SerGluAlATyrAlAlaLeuHISThrLeuThrPheAlaArgProSerSerAlAlaAlaLeu	300
Db	1206	AGCGAGCGCTACGCTCTGCACACTTGTGACCTTCGCGACACCACTCCAGCGCGCTCACTC	1265
Qy	301	AlAlpHeValTrpAlaGlyLeuProGlnGlyThrAlaProAlaGlyThrProAlaTrp	320
Db	1266	CGCTTTGTGTGGGAGAGTTGGCCACAGGAGTGACATCGCGCTCGACACTCCACCTCGG	1325
Qy	321	GlUGlnAlAsnSerGlyGlyTYrTrpLeuThrTrpArgHisAsnGlyTYrThrPheProAla	340
Db	1326	GAGCAGGAGATCTCGGGGGCTACTCTCACTCGGCGCCCAACAGGTACATCTTCCCACT	1385
Qy	341	GLYSerValSerTYrValLeuProGlnGlyPheAlaLeuGluArgTYrAspProAsnAsp	360
Db	1386	GGCTCCGTTAGCTACGTTCTCCCTAAGGTTTGGCCCTTGAAGCGCTACGACCCGAACGAC	1445
Qy	361	GLYSerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnValAlaVal	380
Db	1446	GGCTTTGGACCGACTTGCTCCGCGCAGAGACACCGCTCACTTTCGGCAGAGTCCGCGTC	1505
Qy	381	AspGluValAlaValThrAsnAsnProAlaGlyGlySerAlaProThrPheThrVal	400
Db	1506	GACGAGGTGTGTACCAACAACCCCGCGGCGGAGGAGGCCCACTTCACCGCTG	1565
Qy	401	ArgValProProSerAsnAlaTYrThrAsnThrValPheArgAsnThrLeuLeuGlnThr	420
Db	1566	AGAGTGGCCCTCTTAAAGCGCTTACACAACAACCGTGTTAGGAACACGCTCTTACAGACT	1625
Qy	421	ArgProSerSerArgArgLeuGlnLeuProMetProProAlaAspPheGlyGlnThrVal	440
Db	1626	CGACCTCTCTCGTAGGCTCGAAGCTCCCTATGCCACTGCTGACTTTGGACAGACGCTC	1685
Qy	441	AlaAsnAsnProLYsLlLeGlnSerLeuLeuLYsGlnThrLeuGlyCYsTYrLeuVal	460
Db	1686	GCCAAACAACCCGAAACATGAGAGAGTGGCTTCTTAAAGAAACACTTGGCTGCTATTGGTGC	1745
Qy	461	HisSerLYsMeLArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaVal	480
Db	1746	CACCTCAAAATGCGAAGACCCGTTTTCCAGCTACAGCAGCAGCAGCAGTCTTTGGCGCGCTT	1805
Qy	481	SerPheAsnAsnProGlyTYrGlnArgThrArgAspLeuProAspTYrThrGlyLLeArg	500
Db	1806	TCTCTTCAACAATCCGGGCTTAGAGCGGCACAGCGCACTCCCGGACTACACTGGCATTCGCT	1865
Qy	501	AspSerPheAspGlnAsnMetSerThrAlaAlaHisPheArgSerLeuSerHisSer	520
Db	1866	GACTATTTCGACGAACAATGCTCCACGCGTGTGGCCCACTTCCGCTCACTCTCCACATCC	1925
Qy	521	CysSerLlLeValThrLYsThrTYrGlnGlyTrpGlnGlyValThrAsnValAsnThrPro	540
Db	1926	TGCAGTATCGTCACTAGAACCTTACCAGGGTTGGAGAGCGCTCACGAACGTCAACACGCGCT	1985
Qy	541	PheGlyGlnPheAlaHisAlaGlyLeuLeuLYsAsnGlnGluLlLeLeuCYsLeuAlaAsp	560
Db	1986	TTTCGGCAATTCGGCGACAGCGGCGCTCTCTCAAGATGAGAGATGCTCTGCTCGCGCAC	2045
Qy	561	AspLeuAlaThrArgLeuThrGlyValTYrProAlaThrAspAsnPheAlaAlaAlaVal	580
Db	2046	GACCTGGCGACCGTCTCACAGGTGTCTACCCCGCCACTGCAACAATTCGCGCGCGCTT	2105
Qy	581	SerLlAlaPheAlaAlaAsnMeLLeuSerSerValLeuLYsSerGluAlaThrSerSerLlLe	600
Db	2106	TCTGCTTCGCGGGAACATGCTGTCTCTCGTGTGTAAGTGTGGAGGCAACGCTCTCCATTC	2165

US-09-677-653k-50 (1-647)	x	US-08-485-355b-49 (1-2478)	
QY	1	MetelYspalagIyValAlaserGlnaIgrProHsaBnArGlyThArGsnVal	20
Db	366	ATGGGAATCTCTGGAGTGGGCTACAGCGACCTCAACACGTCGGGAACCCGTAACTT	425
QY	21	ArgYalSerIlaSnPrVAlThrValaSnGlyArGArSngIaBnArGrArGrThGly	40
Db	426	CGGGTCAGCCCAACACCGTCACCGTCATATGGTAGAAGAAACCAACGGGTGGACCGGA	485
QY	41	ArgGlnaIalSerProPoaSpsaSnPheThrAlaAlaIaGlnaIAspLeuAaIagInSerLeu	60
Db	486	AGGCAATTTCTCCCTCGACATTTCCACCGCTGCACAAGACTCTCCGCAAGCCTT	545
QY	61	AspAlaasnThrValThrPheProAlaasnIleSerSerMetProGluPheArGsnTrp	80
Db	546	GACCCCAACACCGTCACCTTTCCCGGTAACTCTACGATCCCGAATTCGGGAATTGG	605
QY	81	AlaIalysIlyslIleAspLeuaspSeraspSerIleGlyTrpTrpY.PheIysTrpLeuasp	100
Db	606	GCCAAAGGAAGATCGACCTCGACTCCGATTCATCGGTGTACTCAAGTAACTTGAAC	665
QY	101	ProAlaGlylaIatHrGlnSerIlaArGAlaIaValGlyIleGlySerIylIleProaspGly	120
Db	666	CCACAGGGGTCTACAGAGTGTGGCGCGCCGTGGGATCTCCGAAGATCCCTCAACGC	725
QY	121	LeuValIysPheSerValAspAlaGluIleargGluIleTyTrasnGluInCySProVal	140
Db	726	CTCGTCAAGTTCTCCGTCGACGAGAGATTAAGAGATCTTAACGAGAGAGTCCCGCTC	785
QY	141	ValIhrAspYalSerValProLeuaspGlyArGlnTrpSerLeuSerIlePheSerPhe	160
Db	786	GTCCTACAGTGTCCGCTCCCGTCGACGGCGGCAATGAGGCTCTCGATTTTCTCTTT	845
QY	161	PrometPheArGrThrAlaTrValAlaAlaAlaAsnValGlnAsnIysGlnmetSerLeu	180
Db	846	CCGATGTTCAGAACCGCTACGTCGCCGCTTAGCAACAGTCGAGAACAGAGATGTCCGTC	905
QY	181	AspYalValaSnaspLeuIleGluTrpLeuAsnAsnLeuAlaAspTrpArGrYalVal	200
Db	906	GACGTTGTCAACACCTCATCGAGTGGCTCAACAATCTCGCGACGCGCTATGTCTGT	965
QY	201	AspSerGlnGlnTrpIleasnPheThrasnAspTrhThTyTrValaIrlaIargIleargVal	220
Db	966	GACCTCAACAGTGGATTAATCTTCACCAATGACACACACTACTACTCCGATCCGATC	1025
QY	221	LeuArGrProThrYalAspValProaspProThGluGlyLeuValArGrThYalSerasp	240
Db	1026	CTACGTCCAACCTACGACGCTTCAGACCCACAGAGGGCTGTTCGCACTCTCAAGAC	1085
QY	241	TyrArGrLeuThrTrYlYsAlaIleThrCysGlnAlaAsnMetProThrLeuValAspGln	260
Db	1086	TACCGCTCACTTATAAGGCGATTAACATGTAAGAACCAATCGCAACACTCTCGACCAA	1145
QY	261	GlyPheTrpIleGlyGlyGlnTrpAlaLeuThrProThSerLeuProGlnTrpAspVal	280
Db	1146	GCGTTTGGATCGCGGCGGACGTACGCTTCACCCGACGATGCTACCGGAGTACGACGTC	1205
QY	281	SerGlnaIaIyAlaLeuHsnIshTrIleuThrPheAlaArGrProSerSerAlaAlaIaleu	300
Db	1206	AGCGAGGCGTACGCTGCGACACTTTGACCTTCGCCAGACATCCAGAGCGCGCTGACAC	1265
QY	301	AlaPheValIrrPaIaGlyLeuProGlnIyGlyThAlaProAlaGlyThProAlaTrp	320
Db	1266	GCGTTTGTGGGAGGTTTGGCCACAGGGTGGGACTGCGCTCGACGGCACTCCACCTGCG	1325
QY	321	GlnaIaIaSerSerGlyGlyTrpLeuThrTrpArGnHsaSnGlyThThThPheProAla	340
Db	1326	GAGGAGGCACTCTCGGGTGGCTACCTGACCTGGCGCCACAAAGGATCACTTCTCCACCT	1385
QY	341	GlySerValSerYalLeuProGluGlyPheAlaLeuGluAlaTrYAspProasnsp	360

Db 1386 GGCCTCCGTTAGCTACCTCTCCCTGAGGGTTTCGCCCTTGAGCGCTACGACCCGGAAGAC 1445
 QY 361 GlysSerThrPheAspPheAlaSerAlaGlyAspThrValThrPheArgGlnValAlaVal 380
 Db 1446 GGCCTTGGACCGACTTCCTCCGACGAGACACCGTCACTTCCGGCAGGTCGCCGTC 1505
 QY 381 AspgLysValValValThrAsnAsnProAlaGlyGlySerAlaProThrPheThrVal 400
 Db 1506 GACGAGGTGTTGTGACCAACACCCGCGGCGGAGCGCCGCCACCTTCACCGTC 1565
 QY 401 ArgValProProSerAsnAlaThrThrAsnThrValPheArgAsnThrLeuLeuGlnThr 420
 Db 1566 AGAGTCCCTCCCTCAACCTTACACCAACACCGTGTAAAGAAACACTTGCTGCTATTGGTGC 1625
 QY 421 ArgProSerSerArgArgLeuGlnLeuProMetProProAlaAspPheGlyGlnThrVal 440
 Db 1626 CAGCCCTCTCTCGTAGGCTCGAACCTCCTATGCCACTTGCTGACTTTGGACAGAGGTC 1685
 QY 441 AlaAsnAsnProLysIleGlnGlnSerLeuLeuLysGlnThrLeuGlyCysTyrLeuVal 460
 Db 1686 GCCAACACCCGACGAGATCGAGCTGCTTAAAGAAACACTTGCTGCTATTGGTGC 1745
 QY 461 HisSerLysMetArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaVal 480
 Db 1746 CACTCCAAATATGGAACCCCGTTTTCAGCTCACGCCACGCTCTTTGGCGCCGCTT 1805
 QY 481 SerPheAsnAsnProGlyTyrGlnArgThrArgAspLeuProAspTyrThrGlyLeuArg 500
 Db 1806 TCCTTCAACATTCGGGTTATGAGCGCACACCGGACTCCCGGACTACACTGGCATCCGT 1865
 QY 501 AspSerPheAspGlnAsnMetSerThrAlaValAlaHisPheArgSerLeuSerHisSer 520
 Db 1866 GACTCATTCGACACGAAATGTCACCGCTGTGCCCACTTCGCTCATCTCCACTCC 1925
 QY 521 CysSerIleValThrThrThrTyrGlnGlyTyrGlnGlyValThrAsnValAsnThrPro 540
 Db 1926 TCGAGTATGCTCACTAGACCTACAGGGTGTGGAAAGCGTCAAGACGTCAACACGCGCT 1985
 QY 541 PheGlyGlnPheAlaHisAlaGlyLeuLeuLysAsnGlnGlnIleLeuCysLeuAlaAsp 560
 Db 1986 TTCGGCCAAATTCGCGACGCGGCGCTCTCAAGAAATGAGAGATCTCTCCCTCGCGCAGC 2045
 QY 561 AspgLeuAlaThrArgLeuThrGlyValTyrProAlaThrAspAsnPheAlaAlaVal 580
 Db 2046 GACCTGGCCACCCGCTCTCAGAGTGTCTACCCGCACTGACAACTTCGCGCGCGCTT 2105
 QY 581 SerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGlnAlaThrSerSerIle 600
 Db 2106 TCTGCCCTTCGCGCAACATGCTCTCTCTGCTAAAGTGGAGGCAACGCTCTTCATC 2165
 QY 601 IleLysSerValGlyGlnThrAlaValGlyAlaAlaGlnSerGlyLeuAlaLysLeuPro 620
 Db 2166 ATCAAGTCCGTTGGCGAGACTCGCGTGGCGGCGCTCACTCCGCGCTCCGGAAGCTACCC 2225
 QY 621 GlyLeuLeuMetSerValProGlyLysIleAlaAlaArgValAlaArgAlaArgAlaArg 640
 Db 2226 GGACTGCTAATAGTGTACAGGAAAGATTGCCGCGCTGTCGCGCGCGGAGGCGGC 2285
 QY 641 ArgArgAlaAlaAlaArgAlaAsn 647
 Db 2286 CGCGCGCGCTGCTGCTCAAT 2306

RESULT 3

US-09-194-613-1
 : Sequence 1, Application US/09194613
 : Patent No. 6251654
 : GENERAL INFORMATION:
 : APPLICANT: GORDON, Karl H.
 : APPLICANT: HANZLIK, Terry N.
 : TITLE OF INVENTION: MODIFIED SMALL RNA VIRUSES
 : NUMBER OF SEQUENCES: 22
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: McDermott, Will & Emery

: STREET: 600 13th Street, N.W.
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20005-3096
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/194,613
 : FILING DATE: 30-NOV-1998
 : CLASSIFICATION: 424
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Bucca Ph.D., Daniel
 : REGISTRATION NUMBER: 42,368
 : REFERENCE/DOCKET NUMBER: 50179-061
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 202-756-8000
 : TELEFAX: 202-756-8087
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2478 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : US-09-194-613-1
 : Alignment Scores:
 : Pred. No.: 0 Length: 2478
 : Score: 3374.00 Matches: 647
 : Percent Similarity: 100.00% Conservative: 0
 : Best Local Similarity: 100.00% Mismatches: 0
 : Query Match: 100.00% Indels: 0
 : DB: Gaps: 0
 : US-09-677-653A-50 (1-647) x US-09-194-613-1 (1-2478)
 QY 1 MetGlyAspAlaGlyValAlaSerGlnArgProHisAsnArgArgGlyThrArgAsnVal 20
 Db 366 ATGGGAGATGCTGGATGGCGCTCACAGCGACCTCACACCGTCCGCGGAACCCGTAACGTT 425
 QY 21 ArgValSerAlaAsnThrValThrValAsnGlyArgArgAsnGlnArgArgThrGly 40
 Db 426 CCGGTACGCGCCCAACACCGCTCACCGTCAATGTATGACAAACCAACGCGCTGGACCGGA 485
 QY 41 ArgGlnValSerProProAspAsnPheThrAlaAlaAlaGlnAspLeuAlaGlnSerLeu 60
 Db 486 AGGCAAGTTTCCCCCTGACAAATTCACCGCTGCGCACAGACCTCGCGCAAGCGCTT 545
 QY 61 AspgAlaAsnThrValThrPheProAlaAsnIleSerSerMetProGlnPheArgAsnThr 80
 Db 546 GACGCCAACACCGCTCACTTCCCGCTAACATCTAGCATCCCGGAATTCGGAATTGG 605
 QY 81 AlalaGlyLysIleAspLeuAspSerSerIleGlyTyrThrPheLysTyrLeuAsp 100
 Db 606 GCCAAGGGAAGATGACTCGACTCCGATTCATCGGCTGCTACTTCAAGTACCTTGAC 665
 QY 101 ProAlaGlyAlaThrGlnSerAlaAlaArgAlaValGlyGlyTyrSerLysIleProAspGly 120
 Db 666 CCAGCGGCTGCTACAGAGTCTCGCGCGCGCTCGCGCGAGTACTCAAGATCCCTACGCGC 725
 QY 121 LeuValLysPheSerValAspAlaGlnIleArgGlnIleTyrAsnGlnGlnCysProVal 140
 Db 726 CTCGTCAAGTCTCCGTGACGACGACAGATTAAGAGATCTATAAGAGAGAGTCCCGCCGTC 785
 QY 141 ValThrAspValSerValProLeuAspGlyArgGlnTyrPheSerLeuSerIlePheSerPhe 160
 Db 786 GTCACTGAGTGTCCGCTCCCTCGACGCGCCGCGAGGCTGTCATTTTCTCCCTTT 845
 QY 161 PrometPheArgThrAlaTyrValAlaValAlaAsnValGlnAsnLysGlnMetSerLeu 180

Db 846 CCGATGTCAGAACCGCCCTACGTCGCCGTAGCGAAGCTGAGACAGAGAGATGTCGCTC 905
 Qy 181 AspValValAsnAspLeuIleGluTyrLeuAsnAsnLeuAlaAspTrrArgTyrValVal 200
 Db 906 GACGTGTCAAGACCTCATCTCGATGCTCAACCAATCTCGCGATCGGCTTATGTCGTT 965
 Qy 201 AASPserGluGlnTrrIleAsnPhenThrAsnAspThrTyrTyrValAlaArgIleAspVal 220
 Db 966 GACTCTGAACAGATGATTAACCTTACCAATGACACACGCTACTACGTCGCAATCCGCGTT 1025
 Qy 221 LeuArgProThrTyrAspValProAspProThrGluGlyLeuValAlaArgThrValSerAsp 240
 Db 1026 CTACGTCCAACCTACGACCTTCCAGACCCACAGAGGCGCTTGTGCACAGCTCAGAC 1085
 Qy 241 TyrArgLeuThrTyrLysAlaIleThrCysGluAlaAsnMetProThrLeuValAspGln 260
 Db 1086 TACCGCTCATTTATAGCGATTAACATGATGAAAGCCACATGCGCAACACTCGTCGACCA 1145
 Qy 261 GlyPheThrIleGlyLysGlnTyrAlaLeuThrProThrSerLeuProGlnTyrAspVal 280
 Db 1146 GGGTTTGGATGGCGGCGGAGTACGCTTCACCCGACCTAGCCTACCGAGTACGACGTC 1205
 Qy 281 SerGluAlaTyrAlaLeuHisThrLeuThrPheAlaArgProSerSerAlaAlaAlaLeu 300
 Db 1206 AGCGAGCGCTACGCTGACACTTGGACCTTCCGACACATCCAGCGCGCTGCACATC 1265
 Qy 301 AlaPheValTrrAlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrProAlaTrr 320
 Db 1266 GGGTTTGTGGGCGAGGTTGGCCACAGGGTGGCAGCTGCGCTGACAGGACATCCAGCGCTG 1325
 Qy 321 GluGlnAlaSerSerGlyLysTyrLeuThrTrrArgHisAspGlyThrThrPheProAla 340
 Db 1326 GAGCAGGCAATCCCGGGTGGCTACCTCACCCTGGCGCCACAGGTAAGTACTCTTCCAGCT 1385
 Qy 341 GlySerValSerTyrValLeuProGlnGlyPheAlaLeuGluArgTyrAspProAsnAsp 360
 Db 1386 GGGTCGTTAGCTAGCTTCTCCCTGAGGGTTTGGCCCTGAGGCGTACGACCGGAAGCAG 1445
 Qy 361 GlySerTrrThrAspPheAlaSerAlaGlyAspThrValThrPheArgIleValAlaVal 380
 Db 1446 GGCTCTTGGACGACTTCTCCCTCCGACGAGACACCGCTCACTTCCGGAGGCGCGCTC 1505
 Qy 381 AspGluValValTrrAsnAsnProAlaGlyGlySerAlaProThrPheThrVal 400
 Db 1506 GACGAGGTGTTGTGACCAACAACCCCGCGGCGGAGCGCCCCACCTTCCACCGTG 1565
 Qy 401 ArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuLeuGluThr 420
 Db 1566 AGAGTCCCCCTTCAAAACGCTTACACCAACACCGCTTAGGAACAACGCTTAGAGACT 1625
 Qy 421 ArgProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGlyGlnThrVal 440
 Db 1626 CGACCCCTCTCTCGTAGGGTCCGAACCTCCATGCCACCTGCTGACAGAGCGTTC 1685
 Qy 441 AlaAsnAsnProLysIleGluGlnSerLeuLeuLysGluThrLeuGlyCysTrrLeuVal 460
 Db 1686 GCCAACACCCGAGATTCAGACAGTGGCTTTTAAAGAAACACTTGGCTGCTATTGGTTC 1745
 Qy 461 HisSerLysMetArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaVal 480
 Db 1746 CACTCCAAATGCGAAGACCCCGTTTCCAGCTCAGCCAGCGACGCTCTTGGCGCGCTT 1805
 Qy 481 SerPheAsnAsnProGlyTrrGluArgThrArgAspLeuProAspTrrArgIleArg 500
 Db 1806 TCCCTTCAACATTCGGGTTATGAGCGCACACGCGACCTCCGCGATACCTGCGATCCGT 1865
 Qy 501 AspSerPheAspGlnAsnMetSerThrAlaValAlaHisPheArgSerLeuSerHisSer 520
 Db 1866 GACTCTATGACCAAGAACTGTCACCGCTGTGGCCACTTCCGCTCACTCTCCACTCC 1925
 Qy 521 CysSerIleValThrLysThrTyrGlnGlyTrrPglGlyValThrAsnValAsnThrPro 540

Db 1926 TGCAATGTCGTAAGACTTACAGAGGTTGGGAAGGCGTCAAGAACTCAACAGCCT 1985
 Qy 541 PheGlyGlnPheAlaHisAlaGlyLeuLeuLysAsnGluGluIleLeuCysLeuAlaAsp 560
 Db 1986 TTCGGCCAAATGCGCAGCCGCGGCTCTTCAAGAAAGAGAGATCTCTGCTCGCGGAC 2045
 Qy 561 AspLeuAlaThrArgLeuThrGlyValTyrProAlaThrAspAsnPhenAlaAlaVal 580
 Db 2046 GACTGGCCACCCGCTCACAGGTGTCTACCCCGCCACATGACAACTTCCGGCGCGCTT 2105
 Qy 581 SerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGluAlaThrSerSerIle 600
 Db 2106 TCGCGCTTGGCGGCAACATGCTGCTCTCGTGTCAAGTCGAGGCAACGCTCTCATC 2165
 Qy 601 IleLysSerValGlyGluThrAlaValGlyAlaAlaGlnSerGlyLeuAlaLysLeuPro 620
 Db 2166 ATCAAGTCGCTGGCGAGACTGCGCGCGCGGCTCACTCCGCGCTCCGGAAGCTACCC 2225
 Qy 621 GlyLeuLysMetSerValProGlyLysIleAlaAlaArgValArgAlaArgAlaArg 640
 Db 2226 GCACTGCTAATGATGTACCAAGGAAATGTCGCGGTGTCCGCGCGCGGAGCGGCC 2285
 Qy 641 ArgArgAlaAlaArgAlaAsn 647
 Db 2286 CGCGGCGCGCTGTCGAAT 2306
 RESULT 4
 US-08-485-355B-51
 ; Sequence 51, Application US/08485355B
 ; Patent No. 6177075
 GENERAL INFORMATION:
 APPLICANT: Christian, P. D., Gordon, K. H.J., Hanzlik, T. N.
 TITLE OF INVENTION: Insect Viruses and Their Uses in
 Protecting Plants
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Flehr Hohbach Test Albritton & Herbert LLP
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/485,355B
 FILING DATE: 07-Jun-1995
 CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/440,522
 FILING DATE: 12-MAY-1995
 APPLICATION NUMBER: US 08/089,372
 FILING DATE: 08-JUL-1993
 APPLICATION NUMBER: AU PL4081/92
 FILING DATE: 14-AUG-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Treccartin, Richard F.
 REGISTRATION NUMBER: 31,801
 REFERENCE/DOCKET NUMBER: A-58631-2/RFT/DSS
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 INFORMATION FOR SEQ ID NO: 51:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2479 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA

FEATURE:
NAME/KEY: CDS
LOCATION: 283..2307
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-08-485-355B-51

Alignment Scores:

Pred. No.:	0	Length:	2479
Score:	3361.00	Matches:	647
Percent Similarity:	99.85%	Conservative:	0
Best Local Similarity:	99.85%	Mismatches:	0
Query Match:	99.61%	Indels:	1
DB:	4	Gaps:	0

US-09-677-653A-50 (1-647) x US-08-485-355B-51 (1-2479)

QY 1 MetGLyAspAlaGlyValAlaSerGlnaTrpOHIsAsnAtrArgGlyThrArgAsnVal 20
DB 366 ATGGGAGATGCTGGAGTGGCGCTCAGAGGACCTCAACCGTGGGGAACCGCTTAACGTT 425
Y 21 ArgValSerAlaAsnThrValThrValAsnGlyArgAsnGlnArgArgThrGly 40
DB 426 CGGGTCACGGCCCAACACCGCTCACCTCAATGTTAGAGAAACCAACGGCGTGGACCGGA 485
QY 41 ArgGlnValSerProProAspAsnPhetThrAlaAlaGlnAspLeuAlaGlnSerLeu 60
DB 486 AGGCAAGTTTCTCCCTGACAAATTTCACCGCTGCTGCACAAAGACCTCGCGCAAGCCTT 545
QY 61 AspAlaAsnThrValThrPhe-ProAlaAsnIleSerSerMetProGluPharAsnTr 80
DB 546 GACGGCAACACCGCTACTTTCCTCCCGCTAACATCTTACACATGCCCCGAATTCCGGAAATTG 605
QY 80 PalAlaSerGlyLysIleAspLeuAspSerAspSerIleGlyTrpYrPheLysTyrLeuAs 100
DB 606 GGCCAAAGGAAGATCGACTCGACTCGATTCATCGGCTGTACTTCAAGTACTTCTGA 665
QY 100 ProAlaGlyAlaThrGlnSerAlaArgAlaValGlyGlnTyrSerLysIleProAspG 120
DB 666 CCCACGGGTGCTACAGAGTGGCGCGCGCTCGCGAGTACTCGAAGATCCTGACGG 725
QY 120 YLeuValLysPheSerValAspAlaGluIleArgGluIleTyrAsnGlnGluLucyProVa 140
DB 726 CCTCTCAAGTCTCCGTCGACGAGATTAAGAGATCTTAACGAGAGATGCCCCGT 785
QY 140 IValThrAspValSerValProLeuAspGlyArgGlnTrpSerLeuSerIlePheSerPh 160
DB 786 CGTCACTACGTCGCTCCCTCGACGGCGCCAGTGGAGCTCTCGATTTTCTCCTT 845
QY 160 eProMetPheArgThrAlaTyrValAlaValAlaAsnValGluAsnLysGluMetSerLe 180
DB 846 TCCGATGTTCAAGAACCGCTACGTCGCGGTAGCGAACGTCGAGAACAGAGATGTCGT 905
QY 180 uAspValValAsnAspLeuIleGluTrpLeuAsnAsnLeuAlaAspTrpArgTyrValVa 200
DB 906 CGACCTTGTCAACGACCTCATCGAGTGGCTCAACAAATCTCGCGCACTGCGCTATGTGT 965
QY 200 LAspSerGlnGlnTrpIleAsnPhetThrAsnAspThrThrTyrTyrValAlaArgVa 220
DB 966 TGACCTTAACAGTGGATTAATCTACCAATGACACCAAGTCTACGTCCTCGATCGGCT 1025
QY 220 LLeuArgProThrTyrAspValProAspProThrGlnGlyLeuValArgThrValSerAs 240
DB 1026 TCTAGCTCCAACTCAGACGTTCCAGACCCCAAGAGGGCGCTGTTCGACAGTCTCAGA 1085
QY 240 pTyrArgGlnThrTyrLysAlaIleThrCysGlnAlaAsnMetProThrLeuValAspG 260
DB 1086 CTACCGGCTCACTAATAAGGGGATTAACATGTGAACCAACAATGCCCAACACTCGTCGACA 1145
QY 260 nGlyPheTrpIleGlyGlnGlnTyrAlaLeuThrProThrSerLeuProGlnTyrAspVa 280
DB 1146 AGGCTTTGGATCGGGCGGCGAGTACGCTCTCAACCCGCACTGACCTTACGCGAGTACGAGCT 1205
QY 280 lSerGlnAlaTyrAlaLeuHisThrLeuThrPheAlaArgProSerSerAlaAlaAla 300

DB 1206 CAGCAGGCGCTACGCTCGACACTTGTGACCTTCCCGACCATCGAGCGCGCTGCACT 1265
QY 300 uAlaPheValTrpAlaGlyLeuProGlnGlyValThrAlaProAlaGlyThrProAlaTr 320
DB 1266 CGGCTTGTGTGGGAGGTTTGGCCACAGGTGGCACTGGCTGGCAGGACTCCAGCTCG 1325
QY 320 pGluGlnAlaSerSerGlyGlyTyrLeuThrTrpArgHisAsnGlyThrThrPheProAl 340
DB 1326 GGAGCAGGATCTCTGGGGTGGCTACTCACTCGGGGCCAACAGGTTACTACTTCCAGC 1385
QY 340 aGlySerValSerTyrValLeuProGlnGlyPheAlaLeuGlnIuaArgTyrAspProAsnAs 360
DB 1386 TGGCTCCGTACTACGTTCTCCCTGAGGGGTTTCCCTTGAGCCCTGACGCCCAAGCA 1445
QY 360 pGlySerTrpThrAspPheAlaSerAlaGlyLysPheThrValThrPheArgGlnValAlaVa 380
DB 1446 CGGCTTGTGGACCGACTTCTGCTTCGCAAGGACACCGCTCACTTTCGGGAGTGGCCGT 1505
QY 380 LAspGluValValAlaThrAsnAsnProAlaGlyGlyGlySerAlaProThrPheThrVa 400
DB 1506 CGACGAGGTCGTTGTGACCAACAAACCCGCGCGGGCGGACGCGCCCACTTACCGCT 1565
QY 400 lArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeuLeuGluTh 420
DB 1566 GAGATGCCCCCTTCAAAAGCTTACACCAACACCGTGTTAGGAACACGCTCTTAGAGAC 1625
QY 420 rArgProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGlnThrVa 440
DB 1626 TCGACCTCTCTCTGTAGGCTTGAACCTCTTAAGCACTGTGATGGACAAACAGCT 1685
QY 440 lAlaAsnAsnProLysIleGlnGlnSerLeuLeuLysGlnThrLeuGlyCysTyrLeuVa 460
DB 1686 CGCCAAACACCGAAGATCGACACTCGCTTTTAAAGAAACACTTGGCTGTATTGTGT 1745
QY 460 lHisSerLysMetArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaVa 480
DB 1746 CCACCTCAAAATGCGAAACCCCGTTTCCAGCTCACCGCACGCACTCTTGTGGCGCGCT 1805
QY 480 lSerPheAsnAsnProGlyTyrGlnArgThrArgAspLeuProAspTyrThrGlyIleAr 500
DB 1806 TTCTTTCAAACAATCCGGGTATAGCGACGACGCAACCTCCCGGACTACACTGGCATCCG 1865
QY 500 gAspSerPheAspGlnAsnMetSerThrAlaValAlaHisPheArgSerLeuSerHisSe 520
DB 1866 TGACTCATTCGACGAGAACATGTCCACCGCTGTGGCCCACTTCCGCTACATCTCCACTC 1925
QY 520 rCysSerIleValThrLysThrTyrGlnGlyTyrpGlnGlyValThrAsnValAsnThrPr 540
DB 1926 CTGCAGTATCGCTACCTAGACCTTACAGAGGTGGGAAAGCGCTCAACGACGCAACGCGC 1985
QY 540 oPheGlyGlnPheAlaHisAlaGlyLeuLeuLysAsnGlnGluIleLeuCysIleuAlaAs 560
DB 1986 TTTTCGGCAATTCGCGCAACGGGGGCTCTCTCAAGATATAGAGATCTCTCTCGCGCA 2045
QY 560 pAspLeuAlaThrArgLeuThrGlyValTyrProAlaThrAspAsnPheAlaAlaAlaVa 580
DB 2046 CGACCTGGCCACCGCTGTACAGAGTGTCTACCCGCGCACTGACAACTTGGGGCGCGCT 2105
QY 580 lSerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGlnAlaThrSerSerIl 600
DB 2106 TTTCTCTCTTCCCGCGCAACATGCTGCTCCGCTGTGAAGTCGAGGACGACGCTCTCAT 2165
QY 600 eIleLysSerValGlyGluThrAlaValGlyValAlaGlnSerGlyLeuAlaLysLeuPr 620
DB 2166 CATCAAGTCCCTTGGCGGAGCTGCGGTGGGGGCTCAAGTCGGGCTCGGGAAGCTACG 2225
QY 620 nGlyLeuLeuMetSerValProGlyLysIleAlaAlaArgValArgAlaArgArgAlaAr 640
DB 2226 CGGATGCTTAATGAGTGTACCAAGGAAAGATTGCCGCGGTCTCCGCGGCGCGGACGCGG 2285
QY 640 gArgArgAlaAlaArgAlaAsn 647
|||||

Db 2286 CCGCGCCGCGCGTGTGCAAT 2307

RESULT 5

US-09-194-613-4

Sequence 4, Application US/09194613

Patent No. 6251654

GENERAL INFORMATION:

APPLICANT: GORDON, KARL H.

APPLICANT: HANZLIK, TERRY N.

TITLE OF INVENTION: MODIFIED SMALL RNA VIRUSES

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: McDermott, Will & Emery

STREET: 600 13th Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3096

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/194,613

FILING DATE: 30-NOV-1998

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Bucca Ph.D., Daniel

REGISTRATION NUMBER: 42,368

REFERENCE/DOCKET NUMBER: 50179-061

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-756-8000

TELEFAX: 202-756-8087

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 6534 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-194-613-4

Alignment Scores:

Pred. No.:	3,226-20	Length:	6534
Score:	294.00	Matches:	184
Percent Similarity:	37.50%	Conservative:	74
Best Local Similarity:	26.74%	Mismatches:	281
Query Match:	8.71%	Indels:	151
	4	Gaps:	35

US-09-677-653a-50 (1-647) x US-09-194-613-4 (1-6534)

QY 2 G1YAspAlaGlyValAlaSerGlnArgProHisAsnArgGlyThrArgAsnValArg 21

Db 4012 GGGCAACAGGGCGCGCAACACACACACAGTGTGACCGACGAGGCGGCTTAA 4071

QY 22 ValSerAlaAsnThrValThrValAsnGlyArgArgAsnGlnArgArgGlyArg 41

Db 4072 CTTCCTCCCGTAGTCGACGCGATT----- 4095

QY 42 GlnValSerProProAspAsnPhetThrAlaAlaGlnAspLeuAlaGlnSerLeuAsp 61

Db 4096 ---ACGAGCCCGCAGATGGCCGACCCGAC-----CAC 4128

QY 62 AlaAsnThrValThrPheProAlaAsnIleSerSerMetProGluPheArgAsnTrpAla 81

Db 4129 GCGAACAACCGGCTCAAC-CCGCGGTG-----GACACGCGTGAAGGGGCT 4172

QY 82 LysGlyLysIleAspLeuAsp-----SerAspSerIleGlyTyrTyrPheLysTyr 98

Db 4173 AAGGCAAGCATGATGAGAGTCCCATGCGACGACATCAAGCATGATGATTCACGACTAT 4232

QY 99 LeuAspProAlaGlyAlaThrGlnSerAlaArgAlaValGlyGluTyrSerLysIlePro 118

Db 4233 CTAGACCCGAGACGAGAAATACACAGACGCTGGACGACG6-----AAATTC 4283

QY 119 AspGlyLeuValLysPheSerValAspAlaGluIleArgGluIleTyrAsnGluGly 138

Db 4284 GACGGCGGATACCTCATGCTACATGCGGTCATATTGGAGGACCGGCGGCGACATAC 4343

QY 139 ProValValThrAspValSerValProLeuAspGlyArgGlnTyrSerLeuSerIlePhe 158

Db 4344 CCGGGAATGATTCAGCAGCTCCCTGGATGGCGGAGCTGCTCTAGTATG 4403

QY 159 SerPheProMetPheArgThrAlaTyrValAlaValAlaAsnValGluAsnLysGluMet 178

Db 4404 CATCTCCGTTCTTCAGCATCCGTTGTTCATCCACACCCAGCACACGGA--- 4460

QY 179 SerLeuAspValValAsn---AspLeu-----IleGluTrpLeuAsnLeu 193

Db 4461 ---CTCAGAGTACGAAACGCGCATCTGATGCTCGCGAAGATGG---AACACAGG 4514

QY 194 AlaAspTrpArgTyrValValAspSerGluGlnIleThrIleAsnPheThrAspThr 213

Db 4515 ACGGACTGGACCGAAGCGAGC---TACCAAGTTGGCGGCAAGTCGGGAAC-----GTG 4565

QY 214 TyrTrpValArgIleArgValLeuArgProThr-----TyrAspValProAspPro 230

Db 4566 TTTTACATGGTCGTC-----CCGACGAAAGCGCTGACGAGGATACACCCCG 4613

QY 231 ThrGlu---GlyLeuValArgThrValSerAspTyrArgLeuThrTyrLysAlaIleThr 249

Db 4614 ACTGATCGGTGTATGAGGTTACTGAGATGATCCGTCGATGATGAGGCGGCTACA 4673

QY 250 CysGluAlaAsnMetProThrLeuValAspGlnGlyPheThrIleGlyGlnTyrAla 269

Db 4674 GCGTACTTCAACGACGACCTCTGTGATGAGGAGTGGCGGATGCGGCACTTC--- 4730

QY 270 LeuThrProThrSerLeuProGlnIleTyrAspValSerGluAlaTyrAlaLeuHisThrLeu 289

Db 4731 ---CAACCGGACAAAGAACACACAGAGAACCCGACATAGTACCGGACCCAA 4787

QY 290 Thr-----PheAlaArgProSerSerAlaAlaAlaLeuAlaPhe 302

Db 4788 ACGGGCGAAGCTTACAGCTCGGCGGTTCAGGCGCAATGACATGACATGACG--- 4844

QY 303 ValTrpAlaGlyLeuProGlnGlyGlyThrAla---ProAlaGlyThrProAlaTrpGlu 321

Db 4845 ATCGGGACACAGTGCAGTTCGGGGCGGACCAATCCCGTACCCAGCGTGTGATGGG 4904

QY 322 GlnAlaSerSerGlyGlyTyrLeuThrTyrArgHisAsnGlyThrThrPheProAlaGly 341

Db 4905 CCGATCCCGGAGTCGGGCGAGCTGTGTCCAGCTCGAAGCTGACATTCGACGTGCGA 4964

QY 342 -----SerValSerTyrValLeuProGlnGlyPheAlaLeuGluArgTyrAspPro 358

Db 4965 AACACATACACATACAGACACAGCTGCCACAGGTCGCGT----- 5006

QY 359 AsnAspGlySerTyrThrAspPheAlaSerAlaGly---AspThrValThrPheArgGln 377

Db 5007 ---ACGGGAATGTGCAATTCCAGCACGACGAGCGGACGCGGACCTGAGCC----- 5054

QY 378 ValAlaValAspGluValValValThrAsnAsnProAlaGlyGlySerAlaProThr 397

Db 5055 -----GTGAC-----GGGGAGCG----- 5069

QY 398 PheThrValArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeu 417

Db 5070 ---ACTGAGCGCTTCGAGAGGATTTGACGCGCTCGAAGTAAATGGAGACATCA 5126

QY 418 LeuGluThrArgProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGly 437

Db 5127 CTCATCAAGATTCACCAAC-----GACATGAACCCAAATGAAGAGCGC 5171

QY 438 GlnThrValAlaAsnAsnProLysIleGluGlnSerLeuLeuLys-GluThrLeuGlyCy 457

```

Db 5172 -----AACGCCAAGACCATTGCTTCCAACTAACGAACGAGCGCATTAATATG 5219
Qy 457 sTYrLeuValHisSerLysMetArgAsnProValPheGluLeuThrProAlaSerSeph 477
Db 5220 CCGC-----AGCGCTCAATCCGCTGTTGGAATGCAAT-GGACGCTTGA 5293
Qy 477 eglYAlaValSerPheAsnAsnProGlyTYrGluArgThrArgAsp----LeuProAspT 496
Db 5264 TGGACCGGTGGAT-----GAAAGACACCGAGAGACAACGTGTGTAATTT 5395
Qy 496 ytrHrGly-----IleArgAspSerPheAspGlnAsnMetSer----- 508
Db 5306 ACACCGCGCAATTGCTGCTACTCCAGAGATACATCGACACACTTGCATAGATTGCC 5365
Qy 509 -----ThrAlaValAlaHis-PheArgSerLeuSerHisSerCysSerIleValThr 525
Db 5366 GTCGATGACCGGTATGCTATCAATCAACCGTACTTCCAAAGTGTTCGACGCTTGC 5425
Qy 526 LysThrTYrGln-GlyTYrPeluGlyValThrAsnValAsnThrProPheGlyGlnPheAl 545
Db 5426 AAGCATACCGGGGAGGAGGAG-----CCTTGGGGCCCTTCCG 5464
Qy 545 aHsAlaGlyLeuLeuLysAsnGluIleLeuCysLeuAlaAspLeuAlaThrAr 565
Db 5465 TACTGGGACACTCCGAAAGACGACGTGGCGCTAACAGTGTGCTGAACCTTGACCGATCT 5524
Qy 565 glauThrGlyValTYrProAlaThrAspPheAlaAlaValSerAlaPheAlaAl 585
Db 5525 GCACCATTCGCAATCCCGAAGCATACACGATTCGGGGCCCTATTCGCGATGTGGC 5584
Qy 585 aAsnMetLeuSerSerValLeuLysSerGluAlaThrSerIleIleLysSerValG 605
Db 5585 CAAGACCATAGCCCAATACCTCGC-----TATGTGGATCA----- 5621
Qy 605 ygluThrAlaValGlyAlaAlaGlnSerGlyLeuAlaLysLeuProGlyLeuLeuMetSe 625
Db 5622 -----GCAGCCGAGGTGGCGAATCGGTGAGCGACTGCATGATAGAGCGCGACCGAG 5674
Qy 625 rValProGlyLysIleAlaAlaArgValArgAlaArgArgAlaArgArg----- 641
Db 5675 TGTAGCTCGAATTCACACCTCGGAGAGCGCGAACGACGACGACGATGTGGCGAAT 5734
Qy 642 ----ArgAlaAlaArg 645
Db 5735 CGCTCGAGGAGCGCG 5750

RESULT 6
US-09-071-035-419
Sequence 419, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: GILL H. CHOI
TITLE OF INVENTION: Enterococcus faecalis polynucleotides and polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071.035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

```

```

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEO ID NO: 419:
SEQUENCE CHARACTERISTICS:
LENGTH: 3695 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-071-035-419

Alignment Scores:
Pred. No.: 0.000308 Length: 3695
Score: 139.50 Matches: 140
Percent Similarity: 31.38 Conservative: 95
Best Local Similarity: 18.698 Mismatches: 247
Query Match: 4.138 Indels: 267
DB: Gaps: 31

US-09-677-653a-50 (1-647) x US-09-071-035-419 (1-3695)

Qy 19 AsnValArgValSerAlaAsnThrValThrValAsnGlyArgAsnGlnArgArg 38
Db 1625 AACCGCAAGTCAACCGAAGCTTGTAACACCAACGCGCCCTAAA----- 1669
Qy 39 ThrGlyArgLysSerProAspAsnPheThrAlaAlaAlaGlnAspLeuAlaGln 58
Db 1670 -----ATCACACGCCCAACAGGTTTCACCCAAAGTAAACAAAGCGATTTACA 1717
Qy 59 SerLeuAspAlaAsnThrVal-----ThrPheProAlaAsnIleSerSer--- 73
Db 1718 AGC---GACCCCTACACATTTCAACAAAGACGACGACCTTACCAACACTTACACAAACAGGC 1774
Qy 74 -----MetProGluPheArgAsnTrpAlaLysGlyLysIleAspLeuAspSer 91
Db 1775 GGTAAAGCTTCAAGTTCAAGTTGTTGTTCAAAAGGCAAGTCCATTCTCAACACATTGACA 1834
Qy 92 IleGlyTrpTrpPheLysTYrLeuAspProAlaGlyAlaThrGluSerAlaArgAlaVal 111
Db 1835 ACT----- 1837
Qy 112 GlyGluTYrSerLysIleProAspGlyLeuValLysPheSerValAspAlaGluIleArg 131
Db 1838 -----ACCAAGCGCCAAAGTTATCAAGTAGCTACGATGACAAATGATGTTTGAAAT 1888
Qy 132 GluIleTYrAsnGluGluCysProValValThrAspValSerValProLeuAsp----- 149
Db 1889 GTGGTGTATGACGAAGAACAACGTTAGACAGTATCATCATGATCATATGAACCTTGTG 1948
Qy 150 -----GlyArgGlnTrpSerLeu 155
Db 1949 AATGAAAAAGCGGCGCTTTCACACCGCGGTAACTTTAGTGTGAAGTACATGCGCAA 2008
Qy 156 SerIlePheSerPheProMetPheArgThrAlaTYrValAlaValAlaAsnValGluAsn 175
Db 2009 AGTACGAGTGCCTAC-----TTAAGAACCGATTATATGACGTGCTCAAAAAATAAT 2062
Qy 176 -----LysGluMetSerLeuAspValAlaAsnAspLeu 186
Db 2063 GGTAAATGGCAATATACGGTAAGTATTAATATGATGATGATGATGATGATGATGATGAT 2122
Qy 187 IleGluTrpLeuAsn----- 191
Db 2123 TTGAAAAAATATATATATGAGACAAACCAATCAGTACCAACAGATTACGTTAATGTT 2182
Qy 191 ----- 191
Db 2183 GATTAATTAGCATGACGACCAACAACTAAATATGTTGACAGCATTCATTAAGACACAGCT 2242

```



```

QY 192 -----AsnleuAlaSerPArgTyrValVal-----200
Db 2243 CAAGAGTCAATCTGAAATCCCTATGATATGTGTACACGACAAATAGCTCAGTTC 2302
QY 201 -----AspSerGluGlnTrpIleAsn 207
Db 2303 GACCCAAATGTAGACACGAGAGTGTGACCTTAGTCAGAATCTGTAACTGCTTAAT 2362
QY 208 PheThrAspThrThrTyr-----215
Db 2363 TTTGATTCAGATGCGACCTATTCTTAATGCAAAATAGACTTTTACACGCATTTA 2422
QY 216 -----ValArgIleArgValLeuArgProThrTyrVal-----227
Db 2423 GGTATATGAGGACACACGAGAGTTAACTCTCTGTAATGTTCTTTTAAAGCCAAA 2482
QY 228 ProAspProThrGluGlnLeuValArgThrValSerAspTyrArgLeuThrTyrIleVal 247
Db 2483 CCGCGGATTAAGTCAAAACTGTCT-----TACAAAGTCACTGCCAAACAA 2527
QY 248 IleThrCysGluAlaAsnMetProThrLeuValAspGlnGlyPheTrpIleGlyGln 267
Db 2528 GTCACC-----GAAAACCTCGTGAT-----GTCAACGGGTGCC 2560
QY 268 TyrAlaLeuThrProThrSerLeuProGlnTyrAspValSerGluAlaTyrAlaLeuHis 287
Db 2561 AAAATACATGCGACCAACAGGCTTCACCCAA-----GATACCAAGTACCAATGAAAC 2611
QY 288 ThrLeuThrPheAlaArgProSerSerAlaAlaLeu-----300
Db 2612 AGTAAACACCTTC---AAGTACACAGCGGCAAAAGCTTTACACGAGCATTAACAGT 2668
QY 301 -----AlaPheValTrpAlaGlyLeuProGlnGlyThrAlaProAlaGlyTrpPro 318
Db 2669 GCGAAAGTCTATACGTTCCAAAGGGGTGTAAAGGGAACCAACAGTACGTTG--- 2725
QY 319 AlaTrpGluGlnAlaSerSerGlyTyrLeuThrTrpArgHisnGlyTrpPhe 338
Db 2726 -----AACAAACACCAACT 2740
QY 339 ProAlaGlySerValSerTyrValLeuProGluGlyPheAlaLeuGluArgTyrAspPro 358
Db 2741 CCAAAGCTCAATGCGAC-----TTTGATGGC 2767
QY 359 AsnAspGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnVal 378
Db 2768 AATGACGATATGACCCCATGTATAGGAAGAAATACCAACAGCTAGTGCACATTAACT 2827
QY 379 AlaValAspGluValValValThrAsnAsnProAlaGlyGlyLeuSerAlaProThrPhe 398
Db 2828 CGACCAAAAGAGAGTGTATGATCGAATACCAATGTAATCTGACCAACAGATGCAAT 2887
QY 399 ThrValArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsnThrLeu 418
Db 2888 ACTAGCAAGACACC-----TTACAAATTCACCTTG 2920
QY 419 GluThrArgProSer---SerArgArgLeuGluLeuPro---MetProProAlaAsp 435
Db 2921 AAAAAGGCGCCCAATTGTCAGCTGTGACAGATCCCGCTTATGAAAGACACCA 2980
QY 436 PheGlyGluThrValAlaAsnAsnProLysIleGluGlnSerLeuLeuGluTrpLeu 455
Db 2981 GAAGGAGAAACGACAAATCAATCCA---GTAAATAGTACCTTTGGACAGAGGGGT 3037
QY 456 GlyCysTyrLeuValHisSerLysMetArgAsnProValPheGlnLeuThrProAlaSer 475
Db 3038 -----CCTTACCAATGCCGCTCTATCGGC 3064
QY 476 SerPheGlyAlaValSerPhe-----AsnAsnProGlyTyrGluArgThr 490
Db 3065 AAAAAGTTTCAAGTCTTTCACAACTCGCGCAACAGGAAACCAACACTGTTTGAAA 3124

```

```

QY 491 ArgAspLeuProAspTyrThrGlyIleArgAspSerPheAspGlnAsnMetSerTrpAla 510
Db 3125 GCAGAACTGTACTATTGGTGTATTAAGATAGTACAGTGAATCACTTC-----3175
QY 511 ValAlaHisPheArgSerLeuSerHisSerCysSerIleValThrLysThrTyrGlnGly 530
Db 3176 -----GTGAGAAATGCTCCAAATGATCAAGAGTATGATACCAACAGCAGCAAGGC 3226
QY 531 TrpGluGlyValThrAsnValAsnThrProPheGlyGlnPheAlaHisAlaGlyLeuLeu 550
Db 3227 TTCATCAGTGTGCCAAGCTTCGAC-----TTGCGCAAGTGGCGCTGCAGGAACTAAG 3280
QY 551 LysAsnGluGlnIleLeuCysLeuAlaAsp-----560
Db 3281 CAACACACAGCTTGAACACAGCGCGGATTAATACGCTACAGCGCACAGGAATCCGTAT 3340
QY 561 -----AspLeuAlaThrArgLeuThrGlyValTyr 570
Db 3341 CTGCGGATTAAGAAACGCAACCAATGGAGCTTAAACAGCCGACTGTACAAACAAA 3400
QY 571 ProAlaThrAspAsnPhe-----AlaAlaAlaValSer 581
Db 3401 TCAGCGACACAGACCTTGCTCTACAGCAGCCGCTTATTTAGGGCGCGCTGTCT 3460
QY 582 AlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGlu-----AlaThrSerSer 599
Db 3461 AGCTTACCAATTACATCAACCAACGAGTTAAAAATAGCGTCCGTACACGAGATGCC 3520
QY 600 IleIleLysSerValGlyGlnTrpAla 608
Db 3521 ATTAGCTTACACCAACACACAGCA 3547

```

RESULT 7
US-09-071-035-417
Sequence 417, Application US/09071035
Patent No. 6448043

GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland

COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2.

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ. ID NO: 417:
SEQUENCE CHARACTERISTICS:
LENGTH: 3840 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-09-071-035-417

Alignment Scores:

Pred. No.:	0.000329	Length:	3840
Score:	139.50	Matches:	140
Percent Similarity:	31.38%	Conservative:	95
Best Local Similarity:	18.69%	Mismatches:	247
Query Match:	4.13%	Indels:	267
DB:	4	Gaps:	31

US-09-677-653a-50 (1-647) x US-09-071-035-417 (1-3840)

```

Oy 19 AsnValArgValSerAlaAsnThrValThrValAsnGlyArgGAsnGlnArgArg 38
Db 1762 AACCCGAAGTCCAGAGAACTTCGTAGACACACAGCGCGTAA----- 1806
Oy 39 ThrGlyArgGlnValSerProProAspAsnPhetThrAlaAlaGlnAspLeuAlaGln 58
Db 1807 -----ATCACACCGCCCAACAGGTTTCACCCCAAGTAA----- 1854
Oy 59 SerLeuAspAlaAsnThrVal-----ThrPheProAlaAsnIleSerSer--- 73
Db 1855 AGC-----GACGCTACACTTCAACACAGAGCAGCAGCTTACAGACACTTACACAGCG 1911
Oy 74 -----MetProGlnPheArgAsnThrAlaLysGlyLysIleAspLeuAspSerSer 91
Db 1912 GGTAAAGCTACACAGTTCACAAAGGTTGGTCAAAAGCCAAAGCTCCATCTACACATTGACA 1971
Oy 92 IleGlyTrpThrPheLysThrLeuAspProAlaGlyAlaThrGlnSerIleArgIleVal 111
Db 1972 ACT----- 1974
Oy 112 GlyIleuTrpSerLysIleProAspGlyLeuValLysPheSerValAspAlaGlnIleArg 131
Db 1975 -----ACCAAAAGCCCAAGTATATCAAGTACCTACAGATGACATGATGATTTGAAT 2025
Oy 132 GluIleuTrpAsnGlnGluCysProValIleThrAspValSerValProLeuAsp----- 149
Db 2026 GTGGTGTGAAGAAAGAAACAGTTCAGACAGTGTATCCATGATGATGAACTTTGTG 2085
Oy 150 -----GlyArgGlnIlePheSerLeu 155
Db 2086 AATGAAAAAGCGGGGCTTTCACACCGCGTTAACTTTAGTGGTAACTAGTATGCGCAA 2145
Oy 156 SerIlePheSerPheProMetPheArgThrAlaTrpValAlaValAlaAsnValGlnAsn 175
Db 2146 AGTACGAGTGCCTAC-----TTAAGAACCGATTTATATGACGTGCTCAAAATAATAT 2199
Oy 176 -----LysGlnMetSerLeuAspValValAlaAsnAspLeu 186
Db 2200 GGTAAATGGCAATATACGGTAAGTATTAATAATGATGATGATGATGATGATGATGAT 2259
Oy 187 IleGluTrpLeuAsn----- 191
Db 2260 TTGAATAAATATTAATTAATGACAAACCAATCAGTGTACCAACAGATTACATTATGTT 2319
Oy 191 ----- 191
Db 2320 GATAAATAGCATGACCAACAACTAAATATGTTGACAGCATTCATTAATAGACACAGCT 2379
Oy 192 -----AsnLeuAlaAspTrpArgTrpValVal----- 200
Db 2380 CAAGTACCAATCTGAAATCTCTATGATATATGTACAGCAACAAATAGCTCACTGGTTTTTC 2439
Oy 201 -----AspSerGluClnIlePheLeu 207
Db 2440 GACCAAAATGTAGACACAGAGGTTGACCTTACTTACGAAATCTCTTACTTGCCTTAAT 2499
Oy 208 PheThrAsnAspThrThrTyTr----- 215
Db 2500 TTGTATTCAGATGACACCTATTTCTAATGCAAAATATAGACTTTTACACGCAATTA 2559
Oy 216 -----ValArgIleArgValIleuArgProThrTyTrAspVal--- 227

```

```

Db 2560 GGATATAGTGGACACACAGAGTAACTATCTTCGTAAATGTTCTTTTAAACGCCAA 2619
Oy 228 ProAspProThrGlnGlyLeuValArgThrValSerAspTrpArgLeuThrTyTrAla 247
Db 2620 CCTGGGATTAAGTCAAAACTTGTTC-----TACAAAGTCTCTGCAAAACAA 2664
Oy 248 IleThrCysGlnAlaAsnMetProThrLeuValAspGlnGlyPheTrpIleGlyGln 267
Db 2665 GTACAC-----GAAAACCTCGTGAT-----GTCAACGCTGCC 2697
Oy 268 TyrAlaLeuThrProThrSerLeuProGlnIleTyTrAspValSerGlnAlaLeuHis 287
Db 2698 AAAATCATCGTACCAACAGCTTACCCCA-----GTAAACCAAGTACCAATGAAC 2748
Oy 288 ThrLeuThrPheAlaArgProSerSerAlaAlaLeu----- 300
Db 2749 AGTAAACCTTC-----AGTACACAGCGGCAAAAGCTTTACACGACGATACTACAGGT 2805
Oy 301 -----AlaPheValTrpAlaGlyLeuProGlnGlyLysThrAlaProAlaGlyThrPro 318
Db 2806 GGCAAAAGTCTATACGTTCCAAAGGTTGATTAAGGAAACCAAGCAAGTACGTTG--- 2862
Oy 319 AlaTrpGlnAlaSerSerGlyGlyTyTrLeuThrTrpArgHisAsnGlyThrPhe 338
Db 2863 -----AACAAACCAACACT 2877
Oy 339 ProAlaGlySerValSerTrpValLeuProGlnGlyPheAlaLeuGlnIleuArgTrpPro 358
Db 2878 CCAAGCTTAATGCGAC-----TTGATGCGC 2904
Oy 359 AsnAspGlySerTrpThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnVal 378
Db 2905 AATGACGATATACCGCCATGATTAAGAAAGAAATACCAACAGTACGTACATTAACT 2964
Oy 379 AlaValAspGlnValValThrAsnAsnProAlaGlyGlyLysSerAlaProThrPhe 398
Db 2965 CGACCAAAAGAGTATGATATGATACCAATGTAATCTGACAAACGATCGAGAT 3024
Oy 399 ThrValArgValProProSerAsnAlaTrpThrAsnThrValPheArgAsnThrLeu 418
Db 3025 ACTACCAAGCACCC-----TTACAAATCTCACCTTG 3057
Oy 419 GluThrArgProSer-----SerArgIleGlnIleuPro-----MetProAlaAsp 435
Db 3058 AAAAAAGTTCAGTTCCTTCAACAACCTGCGCAACAGGAAACCAACACTGTTTGA 3117
Oy 436 PheGlyGlnThrValAlaAsnAsnProLysIleGlnIleuSerLeuLeuLysIleu 455
Db 3118 GAGGAGAAACGACAAATCAATCCCA--GTAAATAGTACACTTGGACACAGAGGGGT 3174
Oy 456 GlyCysTyLeuValHisSerLysMetArgAsnProValPheGlnLeuThrProAlaSer 475
Db 3175 -----CCTTAACCAATGCGCTCTATGCGC 3201
Oy 476 SerPheGlyAlaValSerPhe-----AsnAsnProGlyTyTrGlnArgThr 490
Db 3202 AAAAAAGTTCAGTTCCTTCAACAACCTGCGCAACAGGAAACCAACACTGTTTGA 3261
Oy 491 ArgAspLeuProAspTrpThrGlyIleArgAspSerPheAspGlnAspMetSerThrAla 510
Db 3262 GCAGAGGTTGTATGATGTTGGTATTAAGATATCTACAGTGGATACCTC----- 3312
Oy 511 ValAlaHisPheArgSerLeuSerHisSerCysSerIleValThrLysThrTyTrGlnGly 530
Db 3313 -----GTAGAAATTCGTTCCAAATGATCAAGAAAGTATGATACACGACGAGGC 3363
Oy 531 TrpGlnGlyValThrAsnValAsnThrProPheGlnIlePheAlaHisAlaGlyLeu 550
Db 3364 TTCATCAGAGTGCACAACTTCGAC-----TTCGSCAAAGTGGCGGTGACAGAACTAAG 3417
Oy 551 LysAsnGlnGluIleLeuCysIleuAlaAsp----- 560
Db 3418 CAACAACACAGCTGAAACACACCGCGGATTTACTAGCGTAAACGACACGAAATCCGAT 3477

```

QY 561 -----AspleuAlaThrArgLeuThrGlyValTyr 570
Db 3478 CTGCGGATTAGAAACGCAACCAATTGGAGCTTAACAGCGCACTGTCAACAACAAA 3537
QY 571 ProAlaThrAspAspPhe-----AlaAlaAlaValSer 581
Db 3538 TCAGCGACAGACAGCTTGCCTACAGGACCGCTTATTATTAGGGGGCGCTGTCT 3597
QY 582 AlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGlu-----AlaThrSerSer 599
Db 3598 AGCTTACCAATTACATTCACACCAACCGAGCTGAAATAATACGGTGTACACGAGTGC 3657
QY 600 IleIleLysSerValGlyGluThrAla 608
Db 3658 ATTAGCTTAACAGCAACAACACAGCA 3684

RESULT 8
US-09-199-290-33
; Sequence 33, Application US/09199290
; Patent No. 6255084
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne R.
; APPLICANT: Nielsen, Ruby
; APPLICANT: Lehmebeck, Jan
; TITLE OF INVENTION: Thermostable Glucoamylase
; FILE REFERENCE: 5279,200-US
; CURRENT APPLICATION NUMBER: US/09/199,290
; EARLIER FILING DATE: 1998-11-24
; EARLIER APPLICATION NUMBER: 1557/97
; EARLIER FILING DATE: 1997-12-30
; EARLIER APPLICATION NUMBER: 0925/98
; EARLIER FILING DATE: 1998-07-10
; EARLIER APPLICATION NUMBER: 60/070,746
; EARLIER FILING DATE: 1998-01-08
; EARLIER APPLICATION NUMBER: 60/094,344
; EARLIER FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: 08/979,673
; EARLIER FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 09/107,657
; EARLIER FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 2748
; TYPE: DNA
; ORGANISM: *Talaromyces emersonii*
US-09-199-290-33

Alignment Scores:
Pred. No.: 0.0057 Length: 2748
Score: 125.50 Matches: 103
Percent Similarity: 31.94% Conservative: 58
Best Local Similarity: 20.44% Mismatches: 182
Query Match: 3.72% Indels: 161
DB: 4 Gaps: 23

US-09-677-653a-50 (1-647) x US-09-199-290-33 (1-2748)

QY 40 G1YArgGlnValSerProAspAsn----- 48
Db 1370 GGTAGCGAAMTGAATATATCCGACACAGCGGTACTAATTTGATTCAGACCTCTGGAA 1429
QY 49 -----PheThrAlaAlaAlaGlnAspLeuAlaGlnSerLeuAsp 61
Db 1430 GAAGTAGAAGATCCATCTTCATTCACAAACCGCGTGCACACACCGCGCC-----CTGCTGAA 1486
QY 62 AlaAsnThrValThrPheProAlaAsn-----IleSerSerMetPro 75
Db 1487 GGCATTCACCTGGCACAAGCTGTAACACACGCTCTCAACATCGCTCTCAGGCCCT 1546
QY 76 GluPhe-----ArgAsnTrp----- 80

Db 1547 CAGGTCCGTGTGTTCTCGCATCATCTGACCGGATCGTATGTTCTGGCAACTTTGGT 1606
QY 81 AlaLysGlyLysIleAspLeuAspSerAspSerIleGlyThrPheLysThrLeuAsp 100
Db 1607 GGCAGCGGTGCTTCGCGCAAGAGAGTGAATTCATCTGGGACATTCACACCTTTGAT 1666
QY 101 ProAlaGlyAlaThrGlu-----SerAlaArgAlaValGly 113
Db 1667 CCGCCCGGAGGCTGTGACAGCTGACCTTCACAGCCGTTCGCGCCCTGGCTGGCAAT 1726
QY 114 TyrSerLysIleProAspGlyLeuValLysPheSerValAspAlaGluIleArgGluIle 133
Db 1727 CACAAGGTGAGTACCGAC-----TCGTTCCGAGATATC 1759
QY 134 TyrAsnGluGlyCysProValValThrAspValSerValProLeuAspGlyArg----- 151
Db 1760 TATGCGATCAACTCAGCATCGACAGAGGATGTCGCGTGCAGTTC-----GGCCGTACCT 1816
QY 151 ----- 151
Db 1817 GAGATGTCTACAGGCGGGAACCCCTGTACTGGCCACAGAGCGGCTGCAGACAG 1876
QY 152 -----GlnTrp-----SerLeuSerIlePheSer 159
Db 1877 CTTACGACGCGCATCTACAGTGAAGATCGCTCGATTAAGTATCAGGAGCTTAGT 1936
QY 160 PheProMetPheArgThrAlaTyrValAlaValAlaAsnValGluAsnLysGluMetSer 179
Db 1937 CTGCGATTTTCCAGGATTCATCTACCTCTGCGCCG-----GTGGCAGCATTAATCTGGC 1993
QY 180 LeuAspValValAsnAspLeuIleGluThrLeuAsnMetLeuAlaAspTrp----- 196
Db 1994 TCACAGACTTTCACGACATCATCTCGCCGCTCCAGACATGATGATATCTGAGT 2053
QY 197 -----ArgTyrValValAspSerGlu-----GlnTrp-IleAsnPheThr 209
Db 2054 ATTGTCTAGCTTTTGCTTATGATTCACAGTGAAGAAAAAATGAACTACATCAGT 2113
QY 209 PAsnAspThrThrTyrTyrValArgIleArgValLeuArgProThrArgAspValProAs 229
Db 2114 TCTAGGAAATATATCTCCCTCAGA-----CGGCTCTTACGGAACATTTCT 2161
QY 229 Pro-ThrGluGlyLeuValArgThrValSerAspTyrArgLeuThrTyrLysAla---I 248
Db 2162 CCGTACAGAGCGCATCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2221
QY 248 IeThrCysGluAlaAsnMetProThrLeuValAspGlnGlyPheTrpIleGlyGlnTr 268
Db 2222 TAACCGCTTGGCGCGGACAGACAGTCCGTC----- 2253
QY 268 YrAlaLeuThrProThrSerLeuProGlnTyrAspValSerGluAlaTyrAlaLeuHisT 288
Db 2254 -----CCGTCTTCTGCGGCGGCAAGCTCCGCAAGAGAGCGTCCCTGCTGCT 2302
QY 288 hrLeuThrPheAlaArgProSerSerAlaAlaAlaLeuAlaPheValThrAlaGlyLeuP 308
Db 2303 CTGCCACCTCTGCCAGGCGCCCATATACAGACGCTACCAACACCGTGTGGCAAGCTCTG 2362
QY 308 roGlnGly-----GlyThrAlaProAlaGlyThrProAlaTrpGlnAla 323
Db 2363 GCTCTGGCAGCTCAACACCAACGAGTGGCCCATCAGACACCTCTGCTGCTGCTGCTGCTGCT 2422
QY 323 IAspSerGlyGlyTyrLeuThrTrpArgHisAsnGlyThrPheProAlaGlySerV 343
Db 2423 TGACCTTCGACGAATGCTGACGACCACTTACGCGGAGACATCTACTGCGCGCTCGA 2482
QY 343 alSerTyrValLeuProGluGlyPheAlaLeuGluIleArgTyrAspProAsnAspGlySer 363
Db 2483 TC-----CCGAGCTGGGCACT 2500
QY 363 rPThrAspPheAlaSerAlaGlyAspThrValThrPheArgGlnValAlaValAspGluV 383
Db 2501 GG-----TCCAGCGCGCAGCGCATCCCTCCGCGCG-----GATG 2536

```

QY 383 aValValThrAsnAnProAlaGlyGlySerAlaProThrPheThrValArgValP 403
DB 2537 CTTACACCAACGACACCGCTCTGG-----TACGGACCGCTAAATCTGC 2581
QY 403 roProSerAlaValThrAsnThrValPheArgAsn-----ThrLeuLeuG 419
DB 2582 CCCCTGGCACACGCTTCGAGTACAAAGTCTTCAAAGAACAGACGAGCGGACCATCTGCT 2641
QY 419 luthrArgProSerSerArgArgLeuGluLeuProMetProProAlaAspPheGlyGlnT 439
DB 2642 GGGAGACAGACCCGGAACCGGTGTACACGGTC-----CCAGCGTACTGTGGGCA 2692
QY 439 hrValAla 441
DB 2693 CTACCGCC 2700

RESULT 9
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Alignment Scores:
Pred. No.: 2.4e+03 Length: 4403765
Score: 124.00 Matches: 169
Percent Similarity: 30.968 Conservative: 74
Best Local Similarity: 21.538 Mismatches: 280
Query Match: 3.688 Indels: 263
DB: 4 Gaps: 39

US-09-677-653A-50 (1-647) x US-09-103-840A-2 (1-4403765)
QY 9 GlnAArgProHisAsnArgArg-----GlyThrArgAsnVal---ArgVal 22
DB 3373909 CGCCAAACCCAGCCGCGCTGCACAAACGACCCGGAACACGATAGTGGCGAGACA 3373968
QY 23 SerAlaAsnThrValThrValAsnGlyArgArg-----AsnGlnArg 36
DB 3373969 CGGAATCTGCACCGGTGGGTGGAGAGACCGGATCACCGGTAGCGGAATCATGTGGGG 3374028
QY 37 ATGATGThGlyArgGlnValSerProAspAsnPhe----- 49
DB 3374029 CGGGACCGCGTGGGTCAACGCCCTCCACCGCGCACTGGCGCCGCCAAACCCCTGAGAA 3374088
QY 50 -----ThrAlaAlaGln 54
DB 3374089 CCAGCGTCAGGTCACACGACACTCTTCCTTAGGGCGCTCCACACACCATCTCCCGG 3374148
QY 55 AspLeuAlaGlnSerLeuAspAlaAsnThrValThrPhePro-----Ala 69
DB 3374149 ATTTTGTCTTCAACAGTGTGTAAATAGCTACGATTCACGAGCGGTAGACGACGACGCC 3374208

```

```

QY 70 AsnIleSerSerMetProGluPheArgAsnTrp----- 80
DB 3374209 GCAGATTCCTCACACACCGCGCTGGCAATTGGCCAGCAGCAGCGCGGACGAGGCC 3374268
QY 81 -----AlaGlyGlyLysIleAspLeuAsp 88
DB 3374269 GCCAGCCACACACCAAGCTCTCGCCGACACATCGCTACCGGATCCACCAAC---AGC 3374325
QY 89 SerAspSerIleGlyTrp---TyrPheLysTyrLeuAspProAlaGlyAlaThrGlnSer 107
DB 3374326 GCACGGCATTTGGATGGGGGCCCATCAACCCAGCATCATCCGGCGTGGCCACACAC 3374385
QY 108 AlaArgAlaValGlyLysTyrSerLysIleProAspGlyLeuValLysPheSerValAsp 127
DB 3374386 GCCCGCGCGGTG----- 3374397
QY 128 AlaGluIleArgGluIleTyrAsnGluGlyCys---ProValValThrAspValSerVal 146
DB 3374398 -----TCTAGCGCGCCCGCTTGGCGCTTCGGCC 3374427
QY 147 ProLeuAspGlyArgGlnTrpSerLeuSerIlePheSerPheProMetPheArgThrAla 166
DB 3374428 CCA----- 3374430
QY 167 TyrValAlaValAlaAsnValGluAsnLysGluMetSerLeuAspValAlaAsnAspLeu 186
DB 3374431 -----TCTCGAGCCACATC-----GCCATGCTTGGAC----- 3374460
QY 187 IleGluTrpLeuAsnAsnLeuAlaAspTrpArgTyrValValAspSerGluGlnTrpIle 206
DB 3374461 --TCATGGGTGCCAGACATGCATGATAGGCCGCCAGATCTCTTAGGGCGGTGTC 3374517
QY 207 AsnPheThrAsnAspThrThrTyrTyrValArgIleArgValLeuAspProThrTyrAsp 226
DB 3374518 CACTGG-----GTCGTCACCGCTGATACGTCG 3374544
QY 227 ValPro---AspProThrGluGlyLeuValArgThrValSerAspTrpArgLeuThrTyr 245
DB 3374545 ATCCCGGATGACACCTGCCAAGCACTGGAGACAGACGCGCTGCTACGCGATATCGGCC 3374604
QY 246 LysAlaIleThrCysGluAlaAsnMetProThrIleValAspGlnGlyPheTrpIleGly 265
DB 3374605 CCCAAGCTCTGACGCGTCCCGCATACCGGACATGCTCCCGGCATGAGCATATCCGC 3374664
QY 266 Gly---GlnTyrAlaLeuThrProThrSerLeuProGlnTyrAspValSerGlnAlaTyr 284
DB 3374665 GGATGATGTTGATCATATATGTC-----GACATCAACAACCCCTTT 3374703
QY 285 AlaLeuHisThrLeuThrPheAlaArgProSerSerAlaAlaAlaLeuAlaPheValTrp 304
DB 3374704 TCATTCGAGGACGACACTTTTAAACCCGCGTGTAGCTGGACGC-----GGC 3374751
QY 305 AlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrProAlaTrpGlnAlaSer 324
DB 3374752 GGCGGCAATCGG-CGGCCACAAACGTCGCGCGGCTCCACCAATTTGGCTTGGCGGATAT 3374810
QY 325 SerGlyGlyTyrLeuThrTrpArg-----HisAsnGlyThr 336
DB 3374811 CCAGCAAGGTATTTGACCTTGGGCGCGCGGCGCCACAAACCGGCGCATGCCCTGAACG 3374870
QY 337 -----ThrPheProAlaGly----- 341
DB 3374871 CCGCGCGGACTTCCTTGATGAACAGCTGCGCGACATGCGCTGCTGCGGCTGAC 3374930
QY 341 ----- 341
DB 3374931 CGATGTATGCGCGATCAACCCCGCTTAGCGGCAACGCGGTATGCGAAGCATCAACT 3374990
QY 342 -----SerValSerTyrValLeuProGlnGlyPheAlaLeuGln 354
DB 3374991 GCGGATATGTGGCATCAACAAACATCATCAACATTTCTTCA-----ATTGCAATACCC 3375044
QY 355 ArgTyrAspProAsnAspGlySerTrpThrAspPhe-----AlaSerAlaGlyAsp 371

```



```

Db 1767 GCCACC-----CCAATACCTGGTACAGGCTATGCATACACCTCGCTGTACACCACT 1820
Qy 161 PromethylPheArg-----ThralatyrValAlaValAlaasnValGlu 174
   |||::: |||
Db 1821 CCAGTGTACAGATTCTTGGCATAACAGTATCCTGTAGCTGTACCTGGGATGGA 1880
Qy 175 AsnLysGluMetSerLeuasp-----ValValasnAspLeuile 187
   |||
   |||
Db 1881 CCGAAGCGGAGCGGGAGATTACTGCATTCAGTCCACATTTGTCTCTGTAGATT 1940
Qy 188 -----GluTrpLeuasnAsnLeuAlaAspTrpArgTyrValValaspSerGlu 203
   |||
   |||
Db 1941 CCAAGTTCACAGAGATGCCGCAAAACACACAGATCATCATATGTGGTGCAAT--- 1997
Qy 204 GluTrpLeasnPheThrAsnAspThrThrTyrTyrValArgIleargValLeuArgPro 223
   |||
   |||
Db 1998 -----GCT 2000
Qy 224 ThrTyrAspValProAspProThrGluGluLeuValArgThrValSerAspTyrArgLeu 243
   |||
   |||
b 2001 ACCATATTCAGTCCAAATGGTCACTCTGAG----- 2030
Qy 244 ThrTyrLysAlaIleThrCysGluAlaAsnMetProThrLeuValAspGlnGlyPheTrp 263
   |||
   |||
Db 2031 -----GACGCAAACTCGCCAAATGTTACAGTGCAGTGCCTTTGG 2069
Qy 263 ----- 263
Db 2070 GCGTGGCCAAACACATGAACCTTAAGTGAATGAGACTCTCAGTGGGACA 2129
Qy 264 -----IleGlyGlnTyrAlaLeuThrProThr----- 273
Db 2130 CCTTGGGTTGTGAAATATTTCTGTGATTTGGAGCAATGCGACATTGACATTACT 2189
Qy 273 ----- 273
Db 2190 GTCTGGGCTTGGAGCGGCCCAAGACATCATTTATGCAGAACGGCTACCAATGCC 2249
Qy 274 -----SerLeuProGlnTyrAspValSerGluAlaTyr 284
Db 2250 ACCACACACACCCACAGTTTATTCTCCAAAGCAGCCGGAAGACACCAACCTCCCT 2309
Qy 285 AlaLeuHisThrLeuThrPheAlaIArgProSerSerAlaIleAlaLeuAlaPheValTrp 304
   |||
   |||
Db 2310 ACCTGAAATACAACTGATTTCTGATCCCATACACG----- 2348
Qy 305 AlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrProAlaTrpGlnAlaSer 324
   |||
   |||
Db 2349 ACAGGTCTACCCAGCTTACTACGCTGTACCAACTCACCGCA-----CCTGCACAGC 2402
Qy 325 SerGlyGlyTyrLeuThrThrTrpArgHisAsnGlyThrThrPheProAlaGlySerValSer 344
   |||
   |||
Db 2403 ACAGGCCCACTGTATCCACCGCGGATGTACACACGCCAACACCGCGGCAACAGTCA 2462
Qy 345 TyrValLeuProGlnGlyPheAlaLeuGluArgTyrAspProAsnAspLysSerTrp--- 363
   |||
   |||
Db 2463 GCGCGCATCACG-----GTGACACCAAGTCATCTCATGGGAC 2501
Qy 364 -----ThrAspPheAlaSerAlaGlyAspThrValThrhe--- 375
Db 2502 AACGGCAGAGAAAGTAGAGCCCCCGACATGACACAGCTCCACCTCACCTACGCCCA 2561
Qy 376 ArgGlnValAlaValAspGluValValValThrAsnAspProAlaGlyGlyLysSerAla 395
   |||
   |||
Db 2562 ACCCAAAATGGCACACAGCCCAACCCAGACAGACTACCCCAACCCAAATGCCACACAGC 2621
Qy 396 ProThrPheThrValArgValArgProProSerAsnAlaTyrThrAsnThrValPheArgAsn 415
   |||
   |||
Db 2622 CCCACCCAGAGTAGTACCCCAACCCAAATGCCACACAGC-----CCC 2666
Qy 416 ThrLeuLeuGlnThrArgProSerSerArgGluLeuProMetProProAlaAsp 435
   |||
   |||
Db 2667 ACCTTGGGAAAAACAAATCTCACTCA-----GCAGTACTACCCCAACCCAAATGCC--- 2720

```

```

Qy 436 PheGlyGlnThrValAlaIaasnProLysIleGluGlnSerLeuLeuLysGluThrLeu 455
Db 2721 -----ACAGCCCACTGTG 2735
Qy 456 GlyCysTyrLeuValHisSerLysMetArgAsnProValPheGlnLeuThrProAlaSer 475
   |||
   |||
Db 2736 GGAAAAACAAGCCCAACCTCACAGTCACTACCCCA-----ACCCCAATGCC 2783
Qy 476 SerPheGlyAlaValSerPheAsnAsnProGlyTyrGluArgThrArgAspLeuProAsp 495
   |||
   |||
Db 2784 ACCAGCCCACTTGGGAAAAACAAGCCCACTCACAGTCACTACCCCAACCCCAAT 2843
Qy 496 TyrThrGlyIleArgAspSerPheAsnAsnMetSerThrAlaValAlaHisPheArg 515
   |||
   |||
Db 2844 GGCACCGGCCCTACGTGGGAGAAACAATCCACAGGCAAAATGCCACACACACTTA 2903
Qy 516 SerLeuSerHisSerCysSerIleValThrLys-----Thr 527
   |||
   |||
Db 2904 GAGAGCAACAGTCCCAACCCCACTAGTACCAGCCAAACCAAAATGCACACAGTCTGT 2963
Qy 528 TyrGlnGlyTrpGluGlyValThrAsnValAsnThrProPheGlyGlnPheAlaHisAla 547
   |||
   |||
Db 2964 ACCACAGGCCAACATPACATPACATTCAGTCAACCTTTCATGTCACTGACAGCCAGT 3023
Qy 548 GlyLeuLeuLysAsnGluGluIleLeu-----CysLeuAlaAspAspLeuAlaThrArg 565
   |||
   |||
Db 3024 -----TCAACCCCAAGACATCAGCTCAGCCCTCAGCAGTCAATTCACGTCACT 3074
Qy 566 -----LeuThrGlyValThrProAla-----ThrAspAsnPheAla 577
   |||
   |||
Db 3075 ATGCTTTACTPAACTCCCTCCACCAACAGCTGTGTAATATPAAACAGGTGCACCA 3134
Qy 578 AlaAlaValSerAlaPheAlaIaasnMetLeuSerSerValLeuLysSerLysAlaThr 597
   |||
   |||
Db 3135 GCTCTATCAGACACATCATGTGTCCACAGTGGCCGCAAAACCCGCGCACGACAC 3194
Qy 598 SerSerIleIleLysSerValGlyGluThrAlaValAlaGlnSerGlyLeuAla 617
   |||
   |||
Db 3195 AGCCAA-----GGTACGAGCGCTCGAAGACATTCACATCC 3230
Qy 618 LysLeuPro-GlyLeuLeuMetSerVal-----ProGlyLysIleAlaIaIArgVal 634
   |||
   |||
Db 3231 ACMAAACCGGAGAGTATGTATCTCACAAAGCAGCGCCCCCAAAATGCAACAGTCGCC 3290
Qy 634 IArgAlaArgArgAlaArgArgArg 642
   |||
   |||
Db 3291 CAGGCCCCCACTGGCCAAAGACGG 3315

```

RESULT 11
 PCT-US95-04611A-18
 : Sequence 18, Application PC/US9504611A
 : GENERAL INFORMATION:
 : APPLICANT: Spate, Richard and Jackman, Winthrop, T.
 : TITLE OF INVENTION: Non Splicing Variants of gp350/220
 : NUMBER OF SEQUENCES: 19
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
 : STREET: 5 Palo Alto Square
 : CITY: Palo Alto
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94306
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: PCT/US95/04611A
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:


```

Db 2904 GGAGGAAAGTCCCAACCCCACTAGTACACAGCAACCAAAAAATGCAACAGCTGCTGT 2963
Oy 528 TGTGNGTGTGGLUGLYVALTHRASVALASNTHTPRPHGLYLPHNHAHLSLA 547
Db 2964 ACCACAGGCGCAATACATTAAGTTCACCTTCTTCATCTCACTGAGACCCAGT 3023
Oy 548 GtyleuLeuYsAsnGLUGLULleuLeu-----CysLeuAlaAspAspleuAlaThrArg 565
Db 3024 -----TCAACCCAGAGACACTCAAGCCCTCCACACAGTACATTCACACGTCACAT 3074
Oy 566 -----LeuThrGlyValThyrProAla-----ThraspAsnPhlea 577
Db 3075 ATGCTTTACTACCTCCGCTCACCACAGCTGTGAATAATATACACAGGTGACACCA 3134
Oy 578 AlaAlaValSerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerLunAlaThr 597
Db 3135 GCCTTATCAGCACATCATGTGTCCACCACTTCCGCAAGAACCCGCCAGGACACAC 3194
Oy 598 SerSerIleIleYsSerValGlyLunThraValGlyAlaAlaGlnSerGlyLeuAla 617
Db 3195 AGCCAA-----GGTCAAGGCCCTGGAAACAGTTCACATCC 3230
Oy 618 LysLeuPro-GtyleuLeuMetSerVal-----ProGlyLysIleAlaAlaLargVa 634
Db 3231 ACAAAACCGGGAGGTTAATGTCAACAAAGGACGCGCCCAAAATGCAACGTCGCC 3290
Oy 634 LArgAlaArgAlaArgArgArg 642
Db 3291 CAGGCCCCAGTGGCAAAAGACGG 3315

```

RESULT 12

US-08-783-774-1
Sequence 1, Application US/08783774
Patent No. 6054130

GENERAL INFORMATION:

APPLICANT: Spaete, Richard
TITLE OF INVENTION: Jackman, Winthrop
TITLE OF INVENTION: NON-SPLICING VARIANTS OF
NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/783,774

FILING DATE: 15-JAN-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7682-037

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5931 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: Coding Sequence
LOCATION: 1014...3734
OTHER INFORMATION:
US-08-783-774-1

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Best Local Similarity:	Mismatches:	Query Match:	Indels:	Gaps:
0.0636	121.00	5931	145	69	20.45%	272	3.59%	223	30

US-09-677-653A-50 (1-647) x US-08-783-774-1 (1-5931)

```

Oy 48 AsnPhetHrAlaAlaGlnAspLeuAlaGlnSerLeuAspAlaAsnThrValThrPhe 67
Db 1518 AATATACGGCAGTAGTAGG-----GCACAGGGGCTGGAT-----GTCACGCTA 1562
Oy 68 ProAlaAsnIleSerSerMetProGlnPheArgAsnTrpAlaLysGlyLysIleAspLeu 87
Db 1563 CCCTTAAGTTGCCAAGCTCAGCTCAGACTCGAATTTTCAGC-----GTA 1607
Oy 88 AspSerAspSerIleGlyTrpThyrPheLysTyrLeuAspProAlaGlyAlaThrGlnSer 107
Db 1608 AAACAGAAATCTCGT-----AATGAGATAGAT-----ATTGAGTGT 1646
Oy 108 AlaArgAlaValGlyLunThrasSerLysIleProAspGlyLeuValLysPheSerValAsp 127
Db 1647 ATTATGAGAGATGGCAATATTCACAGTTCGCCGAGACACAAATTTAACTACACC 1706
Oy 128 AlaGlnIleArgGlu-----IleTyrAsnGlnGluCysProVal 140
Db 1707 TGCATGATACGACAGACGATGTTCCACGGGGGGAATTCACATCAACGAGTCCGCTG 1766
Oy 141 ValThraspValSerValProLeuAspGlyArgGlnTrpSerLeuSerIlePheSerPhe 160
Db 1767 GCCACC-----CCAATACCTGGTACAGGATGATGATGATGATGATGATGATGATGAT 1820
Oy 161 PrometPheArg-----ThraIleTyrAlaAlaValAlaAsnValGlu 174
Db 1821 CCAGTGCACGATTTCTTGGCATAATACAGTATCTCTGATGCTGTTTACTGTGGAGATGGA 1880
Oy 175 AsnLysGlnMetSerLeuAsp-----ValValAsnAspLeuIle 187
Db 1881 CCGAAGGGGAGGGGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1940
Oy 188 -----GlnTrpLeuAsnAsnLeuAlaAspTrpArgTyrValValAspSerGlu 203
Db 1941 CCAGCTTCACAGACATCCGACAAACACACACAGACATCATATGTTGGTACAT--- 1997
Oy 204 GlnTrpIleAsnPhetThrasAspThrThrTyrValArgIleArgValLeuArgPro 223
Db 1998 -----GCT 2000
Oy 224 ThrTyrAspValProAspProThrGlnGlyLeuValArgThrValSerAspTyrArgLeu 243
Db 2001 ACCTATTCAGTCCCAATGTCATCTCTGAG----- 2030
Oy 244 ThrTyrLysAlaIleThrCysGlnAlaAsnMetProThrLeuValAspGlnGlyPheTrp 263
Db 2031 -----GACGCAAACTCGCCAAATGTATACAGTACGCTCTTTGG 2069
Oy 263 ----- 263
Db 2070 GCCTGGCCAAACACACTGAAACTGTTTAAGTCAATAGACTCTGCTCGGGGACGA 2129
Oy 264 -----IleGlyLysGlnTyrAlaLeuThrProThr----- 273
Db 2130 CCTTGGGTGTGAAATATTTCTGGTGCATTTGGAGACATCGGACATTTGACATTACT 2199
Oy 273 ----- 273

```


Db 2190 GTCTCGGGTCTGGCAGCGCCCAAGACATATATTCACAGCAGGCTACCAATGCC 2249
 QY 274 -----SerLeuProGlnThrValSerGluAlaTyr 284
 Db 2250 ACCAACAACCAAGGTTATTTCTCCAGGACCCGAGACACCACTCCCT 2309
 QY 285 AlaLeuHisThrLeuThrPheAlaArgProSerSerAlaAlaLeuAlaPheValTyr 304
 Db 2310 ACCTGAAATCAACTGGATTGTCGATCCCAATPACAAG----- 2348
 QY 305 AlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrProAlaTyrGluAlaSer 324
 Db 2349 ACAGGTCTACAGCTCTACTCTACAGTGTCCAACTCAACGCA-----CTGCAAGC 2402
 QY 325 SerGlyLeuThrLeuThrTrpArgHisAsnGlyThrThrPhePheAlaGlySerValSer 344
 Db 2403 ACAGGCCCCCTGATATCCACGGGATGTACACAGCCCAACACCGCGGACAACTCA 2462
 QY 345 TyrValLeuProGlnGlyPheAlaLeuGluArgTyrAspProAsnArgGlySerTrp--- 363
 Db 2463 GGGCGATCAGCG-----CTGACACCAATGCATCTCCATGGGAC 2501
 QY 364 -----ThrAspPheAlaSerAlaGlyAspThrValThrPhe--- 375
 Db 2502 AACGCGACAGAAAGTAAGCCCGGACATGACACGCTCACACCTCACAGTACACCCA 2561
 QY 376 ArgGlnValAlaValAspGluValValThrAsnAsnProAlaGlyGlyGlySerAla 395
 Db 2562 ACCCAAAATGCCACAGCCCAACCCAGCAGTACCCCAACCCAAATGCCACAGC 2621
 QY 396 ProThrPheThrValArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsn 415
 Db 2622 CCCACCCGACAGAGTACTACCCCAACCCCAATGCCACAGC-----CCC 2666
 QY 416 ThrLeuLeuGlnThrArgProSerSerArgArgLeuGlnLeuProMetProProAlaAsp 435
 Db 2667 ACCTTGGGAAACAGTCTCTACTCA---GCAGTACTACCCCAACCCCAATATGCC--- 2720
 QY 436 PheGlyGlnThrValAlaAsnAsnProGlySLeuGlnSerLeuLeuGlyThrLeu 455
 Db 2721 -----ACCAGCCCACTTG 2735
 QY 456 GlyCysThrLeuValHisSerLysMetArgAsnProValPheGlnLeuThrProAlaSer 475
 Db 2736 GGAACAAACAGCCCACTGACAGTACCTACCA-----ACCCCAATGCC 2783
 QY 476 SerPheGlyAlaValSerPheAsnAsnProGlyTyrGluArgThrArgAspLeuProAsp 495
 Db 2784 ACCAGCCCCACCTGGGAAACAAAGCCCACTCAGCAGTACCTACCAACCCCAAT 2843
 QY 496 TyrThrGlyLeuArgAspSerPheAspGlnAsnMetSerThrAlaValAlaHisPheArg 515
 Db 2844 GCCACCGGCTACTGTGGAGAAACAAAGTCCACAGCAATGCCCAACCACTCA 2903
 QY 516 SerLeuSerHisSerLysSerLeuValThrLys-----Thr 527
 Db 2904 GGAAGAAACAGTCCCACTGATTAACAAGCCCAACCAAAATGCAACCACTGCTGT 2963
 QY 528 TyrGlnGlyTyrGlnGlyValThrAsnValAsnThrProPheGlyGlnPheAlaHisAla 547
 Db 2964 ACCAAGGCAACATTAACATTAAGTTCAAGTTCCATTCAGTACAGAGCCAGT 3023
 QY 548 GlyLeuLeuLysAsnGluGluLeu-----CysLeuAlaAspAspLeuAlaThrArg 565
 Db 3024 -----TCAACCCAGAGACACTCAGCCCTCAGCAGTGAATTCACCTCAAT 3074
 QY 566 -----LeuThrGlyValTyrProAla-----ThrAspAsnPheAla 577
 Db 3075 ATGCGTTTACTAATCTCGCTCGCTCAACAGTGTGTAATAATATACAGTACACCA 3134
 QY 578 AlaAlaValSerAlaPheAlaAlaAsnMetLeuSerSerValLeuLysSerGluAlaThr 597
 Db 3135 GCGCTATTCAGACACATCATGTGTCCACAGTTCGCCAGAACCCCGCCAGGACCAACC 3194

QY 598 SerSerIleIleLysSerValGlyGluThrAlaValAlaGlnSerGlyLeuAla 617
 Db 3195 AGCCAA-----GCGTCAAGCCCTGGAAACAGTTCCACATCC 3230
 QY 618 LysLeuPro-GlyLeuLeuMetSerVal-----ProGlyLysIleAlaAlaArgVa 634
 Db 3231 ACAAAACGGGGGAGGTAAATGTCACCAAAAGCAGCGCCCAAAATGCAAGGTGCC 3290
 QY 634 IArgAlaArgAlaArgArgArg 642
 Db 3291 CAGGCCCCCAGTGGCCAAAGACG 3315
 RESULT 13
 US-09-556-706B-1
 ? Sequence 1, Application US/09556706B
 ? Patent No. 6458364
 ? GENERAL INFORMATION:
 ? APPLICANT: Spaele, Richard
 ? APPLICANT: Jackman, Winthrop
 ? TITLE OF INVENTION: NON SPLICING VARIANTS OF GP350/220
 ? FILE REFERENCE: 7682-050-999
 ? CURRENT APPLICATION NUMBER: US/09/556,706B
 ? PRIOR FILING DATE: 2000-04-24
 ? PRIOR APPLICATION NUMBER: 08/783,774
 ? PRIOR FILING DATE: 1997-01-15
 ? PRIOR APPLICATION NUMBER: 08/229,291
 ? NUMBER OF SEQ ID NOS: 19
 ? SOFTWARE: PatentIn version 3.0
 ? SEQ ID NO 1
 ? LENGTH: 5931
 ? TYPE: DNA
 ? ORGANISM: Virus
 ? FEATURE:
 ? OTHER INFORMATION: gp350/220
 US-09-556-706B-1
 Alignment Scores:
 Pred. No.: 0.0636 Length: 5931
 Score: 121.00 Matches: 145
 Percent Similarity: 30.18% Conservative: 69
 Best Local Similarity: 20.45% Mismatches: 272
 Query Match: 3.59% Indels: 223
 DB: 4 Gaps: 30
 US-09-677-653a-50 (1-647) x US-09-556-706B-1 (1-5931)
 QY 48 AsnPheThrAlaAlaGlnAspLeuAlaGlnSerLeuAspAlaAsnThrValThrPhe 67
 Db 1518 AATTAACGGCGAGTAGAGG-----GCACAGGGGCTGAT-----GTCACGCTA 1562
 QY 68 ProAlaAsnLysSerSerMetProGluPheArgAsnTrpAlaLysGlyLysIleAspLeu 87
 Db 1563 CCTTAAGTTGCCAAGCTCAGCTCAAGACTCGAATTCAGC-----GTA 1607
 QY 88 AspSerAspSerIleGlyTrpTyrPheLysTyrLeuAspProAlaGlyAlaThrGluSer 107
 Db 1608 AAAACAGAAATGCTCGGT-----AATGAGATAGAT-----ATTGAGTGT 1646
 QY 108 AlaArgAlaValGlyGluTyrSerLysIleProAspGlyLeuValLysPheSerValAsp 127
 Db 1647 ATTATGAGAGATGGCGAAATTCACAAGTTCTGCCGAGACAACAAAATTAACATAC 1706
 QY 128 AlaGluIleArgGlu-----IleTyrAsnGluGluCysProVal 140
 Db 1707 TGCAGTGGATACGAGACCATGTTCCAGGGGGGAATTTCTCAGATCAAGAGTCCGCTG 1766
 QY 141 ValThrAspValSerValProLeuAspGlyArgGlnTrpSerLeuSerIlePheSerPhe 160
 Db 1767 GCCACG-----CCAATACCTGTGACAGGTATGATCATAACGCTGCTGACACACAGT 1820
 QY 161 ProMetThrArg-----ThrAlaTyrValAlaValAlaAsnValGlu 174

Db	1821	CCAGGTCACGATTTCTTGGCAATACAGTATCCTGTACGTGTTCCTACCTGGGAATGA	1880
Qy	175	AsnLysGluMetSerLeuAsp-----ValValAsnAspLeuIle	187
Db	1881	CCGAAGGCGACGGGGGAGATTACTGCATTCAGTCCACAACTGTGTCTCTCATGAGATT	1940
Qy	188	-----GluTrpLeuAsnAsnLeuAlaAspTrpArgTyrValValAspSerGlu	203
Db	1941	CCAGGTCACAGGACATGCCGACAAACACACACGACATCATCATATGGTGGTCAAAAT---	1997
Qy	204	GlnTrpIleAsnPheThrAsnAspThrThrTyrTyrValArgIleArgValLeuArgPro	223
Db	1998	-----GCT	2000
Qy	224	ThrTyrAspValProAspProThrGluGlyLeuValArgThrValSerAspTyrArgLeu	243
Db	2001	ACSTATTACAGTGCCAATGGTCACTTGAC-----	2030
Qy	244	ThrTyrLysAlaIleThrCysGluAlaAsnMetProThrLeuValAspGlnGlyHerrTrp	263
Db	2031	-----GACGCAAACTCGCCAAATGTTACAGTGCCTGGCTTTGG	2065
Qy	263	-----	263
Db	2070	GCCTGGCCCAACACACTGAACTGAACTTTAATGCAATGGACATCTACCTCGGGGACA	2129
Qy	264	-----IleGlyGlnTyrAlaLeuThrProThr-----	273
Db	2130	CTTTCGGTGTGTGAATAATTTCTGGTGATTCGGACGAACTCGGCATTTGACATTTACT	2189
Qy	273	-----	273
Db	2190	CTCTCGGGCTTGGCACGGCCCCAGACACTATTATACACAGCAAGCGGTACCAATGCC	2249
Qy	274	-----SerLeuProGlnTyrAspValSerGluAlaTyr	284
Db	2250	ACCAACACACACCAAGGTTATATTTCTCCAAAGCACCCGAGAGACACCAACCTCCCT	2309
Qy	285	AlaLeuHisThrLeuThrPheAlaArgProSerSerAlaAlaLeuAlaPheValTrp	304
Db	2310	ACSTTGAATACAACTGGATTTGGTGTGATCCCAATACAAAG-----	2348
Qy	305	AlaGlyLeuProGlnGlyGlyThrAlaProAlaGlyThrProAlaTrpGlnAlaSer	324
Db	2349	ACAGGTATCCACACTCTACTACAGTGCCTACACCAACCTCACCGCA-----CTTCCAAAG	2402
Qy	325	SerGlyGlyTyrLeuThrTrpArgHisAsnGlyThrThrPheProAlaGlySerValSer	344
Db	2403	ACAGGCCCCACGTGATCCACCGGGGATGTCCACAGCCCAACGCGGACACACGTCA	2462
Qy	345	TyrValLeuProGlnGlyPheAlaLeuGluArgTyrAspProAsnAspLysTrp---	363
Db	2463	GAGCGATCACCG-----GTGCACACCAAGTCATCTCATGGGAC	2501
Qy	364	-----ThrAspPheAlaSerAlaGlyAspThrValThrPhe---	375
Db	2502	AACGGCAGAAAGTAAGCCCCCGGACATGACAGTCCACCTCCACAGTGCATCCCCA	2561
Qy	376	ArgGlnValAlaValAspGluValValThrAsnAsnProAlaGlyGlyGlySerAla	395
Db	2562	ACCCCAATGTCACACAGCCCCACCCACGACGTGACTACCCCAACCCCAATGCCCACAGC	2621
Qy	396	ProThrPheThrValArgValProProSerAsnAlaTyrThrAsnThrValPheArgAsn	415
Db	2622	CCCAACCCACAGAGTACTACCCCAACCCCAATAGCCACAGC-----CCC	2666
Qy	416	ThrLeuLeuGlnThrArgProSerSerArgArgLeuGluLeuProMetProProAlaAsp	435
Db	2667	ACCTTGGGAACAAAGTCTTACTCTCA---GCAGTGTACTACCCCAACCCCAATAGCC---	2720
Qy	436	PheGlyGlnThrValAlaAlaAsnAsnProLysIleGluGlnSerLeuLeuLysGluThrLeu	455


```

Db 366425 GCTTCTTCAACAGCGCGCGGAGGATTCGGAATTCCTGAACCTCCGCTCCGCGCTGT 366366
QY 589 eSerValLeuLysSerGluAlaThrSerSerIleLeuLysSerValGluThrAlaV 609
Db 366365 CGGGCTACTCAATACCGCGCGGCTGGATCGGTCTCCCAACGGGGCAACACCATCT 366306
QY 609 aGlyAlaAlaGlnSerGlyLeuAlaLysLeu-----ProGlyLeuLeuMetSerVal- 626
Db 366305 CGGGCTGTTGAACGACGCGCGCTGATCTCGCAACCGCGGGGTCTCTCCGCGCATCG 366246
QY 627 -----ProG 628
Db 366245 GTAATTGGCACCAACTGGCGGTTCTTTAGGGGATTAACGCGACGATATGCACCTG 366186
QY 628 lYLeuIleAlaAla-----ArgValArgAla-----ArgAlaAla 640
Db 366185 GGCACGACCGCTTCACTGCTCTCCAGAGGTGCAACGCGCTTGGCCGATCTAGACTC 366126
QY 640 rGArgArg 642
Db 366125 GCGCGAAG 366118

RESULT 15
US-09-103-840A-1/c
: Sequence 1, Application US/09103840A
: Patent No. 6294328
: GENERAL INFORMATION:
: APPLICANT: FLEISCHMAN, Robert D.
: APPLICANT: WHITE, Owen R.
: APPLICANT: FRASER, Claire M.
: APPLICANT: VENTER, John C.
: TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
: FILE REFERENCE: 24366-20007_00
: CURRENT APPLICATION NUMBER: US/09/103,840A
: CURRENT FILING DATE: 1998-06-24
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 4411529
: TYPE: DNA
: ORGANISM: Mycobacterium tuberculosis
: OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 5.02e+03 Length: 4411529
Score: 121.00 Matches: 182
Percent Similarity: 31.25% Conservative: 63
Best Local Similarity: 23.21% Mismatches: 283
Query Match: 3.59% Indels: 260
DB: 4 Gaps: 40

US-09-677-653a-50 (1-647) x US-09-103-840A-1 (1-4411529)
QY 31 gLyArGArGAsnGlnArGArGThrGlyArgGlnValSerProAspAsnPhetThr 50
Db 368152 GGGCAAGCTCAACACCGGCTGGCAACACCGGCGACGA-TCAACACCGGCAACATCAACA 368094
QY 51 AlAlaAlaGlnAspLeuAlaGlnSerLeuAspAla-----AsnThrValThrPhe 67
Db 368093 CCGGCAAGCTCAACACCGGCAACATACCGGAGCTTCAACCTCGGCGATCAACA 368034
QY 68 ProAlaAsnIleSerSerMetPro----- 75
Db 368033 CCGGCA-----GCTTCAACTCCGCTGACTACACACCGGCTACTTCAACCGGCTGACT 367980
QY 76 GluPheArGAsnTrpAlaLysGlyLysIleAspLeuAspSerAspSerIleGlyTrpTrpYr 95
Db 367979 ACAACACGCGGTGGCGCAACGCGCAACGTCACACCGGCGCGCTTCA----- 367932
QY 96 PheLysTrpLeuAspProAlaGlyAlaThrGlnSerAlaArgAlaValGlyLysTrpSer 115

```

```

Db 367931 -----TCATCCGCAATTACAGCAACGCGGTTCTTGGCGA-GGTACTAC----- 367888
QY 116 LysIleProAspGlyLeuValLysPheSerValAspAlaGluIleArgGluIleTrpAsn 135
Db 367887 -----CAGGGTTGATGTCCTTCCACACAGCATCAACCATCCGAAATTC----- 367843
QY 136 GluLysCysProValValThrAspAlaSerValProLeuAspGlyArgGlnTrpSerLeu 155
Db 367842 -----CCCTACCGCTACGACTTGAAGTGTTCACATGAC-----ATA 367807
QY 156 SerIle-----PheSerPheProMetPheArg 164
Db 367806 CCCATCACCGGACCGCTGCTGCCACACCCCAACAGTTTCACCATTCGCCGTTTCCAG 367747
QY 165 -----ThrAlaTrpValAlaValAlaAsnValGluAsnLysGluMet-----Ser 179
Db 367746 ATACGAGTTCTGCTGCTGCTCCGCGGCTGCTGTCACAGCATATGATCGGCCCATCACG 367687
QY 180 LeuAspVal-----ValAsnAspLeuIleGlu-TripLe 190
Db 367686 ATCGATGTCATCAAGTCATGCCATCGCATTCGCCCATTCACCAACCATCGATGTTG 367627
QY 190 uAsnAsnLeuAlaAspTrpArgTrpValValAspSerGluGlnTrpIleAsnPhetThrAs 210
Db 367626 GGCACCGCGGCTGCGCGCGATCCCATCGCATCGCATCGGTGTAACCCGCGGTTTC 367567
QY 210 nAspThrThrTrpTrpValArgIleArgValLeuArgProThrTrpAspValProAspTr 230
Db 367566 GGCACCTGCAACCGCGCGCGCTGCGGT-----TCTTCCACACCGCGGCC 367519
QY 230 oThrGluGlyLeuValArgThrValSerAspTrpArgLeu-----ThrTrpLysAlaI 248
Db 367518 G-----GCCATGATCGGGCTTCGGGAGTTCCGGCGCCCGCC 367483
QY 248 eThrCysGluAla-----AsnMetProThrLeuValAspGlnGlyPheTrpIleGlyGly-- 266
Db 367482 AACATGCGGCTCGCGGAACCTTCGCGCTGCG-AATTCGCGGCTCTTTAACGCGCGCG 367424
QY 267 -----GlnTrpAlaLeuThrProThrSerLeuProGlnTrp-- 278
Db 367423 CTGGGCAATTGGGCTTCACTGAAATTTGCGCGCGCTGCAGTGGCTTGGCGCAACCTGG 367364
QY 279 -----AspValSerGluAlaTrpAlaLeuHisThrLeuThrPheAlaArgProSerSerAl 297
Db 367363 CAACACATCTCGGCGCTCAACACGACGACGTGACCTCGGACCGCGCGCTTGG 367304
QY 297 aAlaAlaLeuAlaPheValTrpAlaGlyLeu-ProGln-----GlyGlyThrAlaProAla- 315
Db 367303 CTCGGGCAATCGCAACATCGGCGCCACACCTGCGCTGTTCCTCGACACACCGCGCA 367244
QY 315 ----- 315
Db 367243 CTTGACGCTGAACCTTGGCGCTCGCAACACGCGCGCTCAACCGCGGCAATCGGCAACCT 367184
QY 316 -----GlyThrProAlaTrpLeuGlnAlaSer 325
Db 367183 GGGCAGCGCAACATCGGCTTGTTAATACGGGCGATCCCAACCTGAGGCAATCGGCAACT 367124
QY 325 eRgLyGlyTrpLeuThrTrpArgHisAsnGlyThrPheProAlaGlySerValSerT 345
Db 367123 CG-----GCGACCTCAACTTCGCGCGGCGGCAACATCGG 367091
QY 345 yTrValLeuProGluGlyPheAlaLeuGluAlaGlyTrpAspProAsnAspLysSer----- 362
Db 367090 CGGTAAACAATCGGCA-----TCGCCAACAACCGGATCTTCGATAT 367049
QY 363 -----TriPThrAspPheAlaSer----- 368
Db 367048 CGGCTTGGCAACTGGCGACGCTACACATCGGCTTGGCAATCTGGCGCGACGACACACT 366989
QY 369 -----AlaGlyAspThrValThrPheArgGlnValAla----- 379

```

Db 366988 GGGCTTTGGCAACGGCGAGCTACAAATCGGCTTCGGACTCGCAGCAACT 366929
QY 380 -----ValaspGluValValThrAsnAsp 389
Db 366928 GGGCTTTGCCAACCGGAGCTACAAATCGGCTTCGGCAATACGGTAACAACAT 366869
QY 389 roAlaGlyGlySerAlaProThrPheThrValArgValProProSerAsnAlaTyrT 409
Db 366868 CGGCGTCGGGCTCACCAGCGCAACCGGATCGGATCGGACCTCAACTCGGCGCA 366809
QY 409 hrAsnThrValPheArgAsnThrLeuLeuGluThrArgProSerSerArgArgLeuGlu- 428
Db 366808 CAACATCGGCGCTTCACTCCGAGCGAACAATCGGCTTCTCAACTCGGCGACCG 366749
QY 429 -----LeuProMetProProAlaAspPheGlyGlnThrValAlaAsnA 443
Db 366748 CAACGTGGCATCTTAACACCGCGCAACTTCGGCTCGCAACTCGGCGGCTT 366689
QY 443 snProLysIleGluInsLeuLeuLysGluThrLeuGlyCysTyrLeuValHisSerL 463
Db 366688 CAACACCGGATCGGCAACCGGCGAGCAACACCGGCGGTTCACCCCGGGAGCT 366629
QY 463 ysketaArgAsnProValPheGlnLeuThrProAlaSerSerPheGlyAlaValSerPheA 483
Db 366628 CA-----ACACCGGAGCTTCAACCCGGGAGCTTCAAC-A 366594
QY 483 sn-----AsnProGlyTyrGluArgThrArgAspLeu-----ProAspTyr---T 497
Db 366593 CCGGCGGCTTCAACCGGCGAGTGGCAACACCGGCTACCTCAACACCGGCTACACAA 366534
QY 497 hrGlyIleArgAspSerPheAspGlnAsnMetSerThrAlaValAlaHisPheArgSerL 517
Db 366533 CCGGCGTGGCGAACACGGGAGTGTGACACCGGTCG-----TTCATTACCG 366486
QY 517 euSerHisSerCysSer---IleValThrLysThrTyrGlnGlyTyrGluGlyValThrA 536
Db 366485 GCAGTACAGACAGCGCTTCTGTGTGGTGCACATACAGGCGCTGATCGGCTGGCG 366426
QY 536 snValAsnThrProPhe-----GlyGlnPheAlaHisAlaGlyLeuLeuLysAsnGluG 554
Db 366425 TGTGGGCAATTCGGTACCCCGGCTACTTC----- 366394
QY 554 IuIleLeuCysLeuAlaAspAspLeuAlaThrArgLeuThrGlyValTyrProAlaThrA 574
Db 366393 -----AACCTCACTGGC---GGCCGCTGTCGG 366369
QY 574 spAsnPhe-----AlaAlaAlaValSerAlaPhe-----AlaAlaAsnMetLeuS 589
Db 366368 GCTTTTCAACAGCGCGCGGAGGTATCGGATTCGTGAACCTCGGTCGGGCTGT 366309
QY 589 erSerValLeuLysSerGluAlaThrSerSerIleIleLysSerValGlyGluThrAlaV 609
Db 366308 CCGGCTACCTCACTACCGGCGCTGGATCGGTCGCCAACGTGGCAACACCATCT 366249
QY 609 alGlyAlaAlaGlnSerGlyLeuAlaLysLeu-----ProGlyLeuLeuMetSerVal- 626
Db 366248 CGGCGTGGTGAACGCCAGCGGCTGTGATTCGCCAGCGGCGGCTTCTTCGGCATCG 366189
QY 627 -----Prog 628
Db 366188 GTAACCTTGGCAACCACTGCGGTTTCTTAGGGATTAACGCGCATATGTCACTG 366129
QY 628 LyrLysIleAlaAla-----ArgValArgAla-----ArgArgAlaA 640
Db 366128 GGCACAGAGCGCTTCACTGCTCCAGAGTGAAGCGCCTTTGCCGATCGTAGACTC 366069
QY 640 rgaArgArg 642
Db 366068 GCGGGAAG 366061

